

|  |        |           |           |         |  |   |  |  |  |                 |
|--|--------|-----------|-----------|---------|--|---|--|--|--|-----------------|
|  |        |           |           |         |  | /ug=Hs.81771 /len=1637  |  |  |  |                 |
| GAPD<br>(glyceraldehyde-3-phosphate<br>dehydrogenase)                        | M33197 | Hs.169476 | NM_002046 | 12p13   |  | Homo sapiens /REF=M33197<br>/DEF=Human glyceraldehyde-3-phosphate<br>dehydrogenase (GAPDH) mRNA,<br>complete cds /LEN=1268 (5'_M, _3'<br>represent transcript regions 5 prime,<br>Middle, and 3 prime respectively) |  |  |  | AFFX-HUMGAPDH/M |
| CTNNAL1 (catenin (cadherin-associated<br>protein), alpha-like 1)             | U97067 | Hs.58488  | NM_003798 | 9q31.2  |  | Cluster Incl. U97067:Homo sapiens alpha-<br>catenin-like protein mRNA, complete cds<br>/cds=(43,2247) /gb=U97067 /gi=3342777<br>/ug=Hs.58488 /len=2446  |  |  |  | 35331_at        |
| GNA15 (guanine nucleotide binding protein (G<br>protein), alpha 15 (Gq class | M63904 | Hs.73797  | NM_002068 | 19p13.3 |  | Cluster Incl. M63904:Human G-alpha 16<br>protein mRNA, complete cds<br>/cds=(219,1343) /gb=M63904 /gi=182891<br>/ug=Hs.73797 /len=2060  |  |  |  | 40365_at        |

|   |          |           |           |             |   |          |
|---|----------|-----------|-----------|-------------|---|----------|
| KCNAB2 (potassium voltage-gated channel, shaker-related subfamily, beta member 2) | AF044253 | Hs.298184 | NM_003636 | 1p36.3      | Cluster Incl. AF044253: Homo sapiens potassium channel beta 2 subunit (HK\beta2.2) mRNA, alternatively spliced, complete cds /cds=(0,1061) /gb=AF044253 /gi=2827465 /ug=Hs.154417 /len=1062 | 31901_at |
| TARS (threonyl-tRNA synthetase)   | M63180   | Hs.84131  | NM_003191 | 5p13-cen    | Cluster Incl. M63180: Human threonyl-tRNA synthetase mRNA, complete cds /cds=(138,2276) /gb=M63180 /gi=339679 /ug=Hs.84131 /len=2644  | 38473_at |
| UQCRFS1 (ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1)      | L32977   | Hs.3712   | NM_006003 | 19q12-q13.1 | Cluster Incl. L32977: Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRFS1) gene /cds=(90,914) /gb=L32977 /gi=488298 /ug=Hs.3712 /len=1203     | 34401_at |
| ONECUT3 (one cut domain, family member 3)   | AC004755 |           |           | 19          | Cluster Incl. AC004755: Homo sapiens chromosome 19, fosmid /cds=(0,2726) /gb=AC004755 /gi=3165405   | 33685_at |

|  |        |           |           |             |  |   |                 |  |  |  |
|--|--------|-----------|-----------|-------------|--|---|-----------------|--|--|--|
|  |        |           |           |             |  | /ug=Hs.184922 /len=2727   |                 |  |  |  |
| GAPD<br>(glyceraldehyde-3-phosphate<br>dehydrogenase)  | M33197 | Hs.169476 | NM_002046 | 12p13       |  | Homo sapiens<br>/DEF=Human glyceraldehyde-3-phosphate<br>dehydrogenase (GAPDH) mRNA,<br>complete cds /LEN=1268 (5' _M_ _3<br>represent transcript regions 5 prime,<br>Middle, and 3 prime respectively) | AFFX-HUMGAPDH/M |  |  |  |
| MAX (MAX protein)  | X60287 | Hs.42712  | NM_002382 | 14q23       |  | X60287<br>/FEATURE=cds<br>/DEFINITION=HSMAXM H.sapiens max<br>mRNA  | 1981_s_at       |  |  |  |
| SH3GL1 (SH3-domain GRB2-like 1   | X99656 | Hs.97616  | NM_003025 | 19p13.3     |  | Cluster Incl. X99656:H.sapiens mRNA for<br>protein containing SH3 domain, SH3GL1<br>/cds=(15,1121) /gb=X99656 /gi=1869809<br>/ug=Hs.97616 /len=2349   | 39159_at        |  |  |  |
| SFPQ (splicing factor proline/glutamine rich<br>(polypyrimidine tract-binding protein-<br>associated)) | W27050 | Hs.180610 | NM_005066 | 1pter-p32.3 |  | Cluster Incl. W27050:1977 Homo sapiens<br>cDNA /gb=W27050 /gi=1306422<br>/ug=Hs.180610 /len=699   | 41199_s_at      |  |  |  |

|  |          |           |           |              |   |            |
|--|----------|-----------|-----------|--------------|---|------------|
| PPP6C (protein phosphatase 6, catalytic subunit)                           | X92972   | Hs.80324  | NM_002721 | xq22.3       | Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,938) /gb=X92972 /gi=5701862 /ug=Hs.80324 /len=1292         | 37581_at   |
| HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)) | L24521   | Hs.89525  | NM_004494 | xq25         | Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240 | 36446_s_at |
| ACTG1 (actin, gamma 1)   | X04098   | Hs.14376  | NM_001614 | 17q25        | Cluster Incl. X04098:Human mRNA for cytoskeletal gamma-actin /cds=(73,1200) /gb=X04098 /gi=28338 /ug=Hs.234733 /len=1918          | 34160_at   |
| FBX07 (F-box only protein 7)   | AL050254 | Hs.5912   | NM_012179 | 22q11.2-qter | Cluster Incl. AL050254:Novel human gene mapping to chromosome 22 /cds=(205,1773) /gb=AL050254 /gi=4886422 /ug=Hs.5912 /len=2075   | 35337_at   |
| SCML2 (sex comb on midleg (Drosophila)-like 2)                             | Y18004   | Hs.171558 | NM_006089 | xp22         | Cluster Incl. Y18004:Homo sapiens mRNA for SCML2 protein /cds=(91,2193)   | 38518_at   |



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|--|--------|-----------|-----------|----------|---|-----------|---|--|--|--|--|
|  |        |           |           |          |   |           | /gb=Y18004 /gi=4480941 /ug=Hs.171558<br>/len=4130 |  |  |  |  |
| UBE2L3 (ubiquitin-conjugating enzyme E2L                                     | S81003 | Hs.108104 | NM_003347 | 22q11.21 | S81003<br>/DEFINITION=S81003 - L-UBC=ubiquitin<br>conjugating enzyme [human, odontogenic<br>keratocysts, mRNA Partial, 683 nt]                                  | /FEATURE= | 223_at  |  |  |  |  |
| GNAQ (guanine nucleotide binding protein (G<br>protein), q polypeptide       | U40038 | Hs.296261 | NM_002072 | 9q21     | Cluster Incl. U40038:Human GTP-binding<br>protein alpha q subunit (GNAQ) mRNA,<br>complete cds /cds=(42,1121) /gb=U40038<br>/gi=1181670 /ug=Hs.180950 /len=1450 |           | 38581_at  |  |  |  |  |
| UGTREL7( UDP-glucuronic acid/UDP-N-<br>acetyl/galactosamine dual transporter | D87449 | Hs.82635  | NM_015139 | 1        | Cluster Incl. D87449:Human mRNA for<br>KJAA0260 gene, partial cds /cds=(0,1153)<br>/gb=D87449 /gi=1665786 /ug=Hs.82635<br>/len=5918                             |           | 37888_at  |  |  |  |  |

Table 12:

| UC/L/HGNC/HUGO Human Gene Nomenclature<br>Database Symbol                       | GenBank<br>Accession No. | UniGene Cluster | RefSeq    | Chromosomal<br>Location | Description Unigene Build #95  | Gene Name |
|---|--------------------------|-----------------|-----------|-------------------------|--|-----------|
| KIAA0101( KIAA0101 gene product )   | D14657                   | Hs.81892        | NM_014736 | 15                      | Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds<br>/cds=(61,396) /gb=D14657 /gi=285938<br>/ug=Hs.81892 /len=836    | 38116_at  |
| IGFBP7 (insulin-like growth factor binding protein 7)                           | L19182                   | Hs.119206       | NM_001553 | 4q12                    | L19182<br>/DEFINITION=HUMMAC25X Human<br>MAC25 mRNA, complete cds  | 2062_at   |
| RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)) | X55988                   | Hs.728          | NM_002934 | 14q24-q31               | Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin<br>/cds=(71,556) /gb=X55988 /gi=31088<br>/ug=Hs.728 /len=735 | 36766_at  |

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|--|----------|-----------|-----------|--------------|---|-----------------|
| SCYC2 (small inducible cytokine subfamily C, member 2) | D63789   | Hs.174228 | NM_003175 | 1q23-q25     | Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor, complete cds /cds=(21,365) /gb=D63789 /gi=1754608 /ug=Hs.174228 /len=485   | 31495_at        |
| DEFA1 (defensin, alpha 1, myeloid-related sequence)    | AL036554 | Hs.274463 | NM_004084 | 8p23.2-p23.1 | Cluster Incl. AL036554:DKFZp584J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp584J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517  | 31793_at        |
| GAPD (glyceraldehyde-3-phosphate dehydrogenase)        | M33197   | Hs.169476 | NM_002046 | 12p13        | Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 /5'_M_3 represent transcript regions 5 prime, Middle, and 3 prime respectively) | AFFX-HUMGAPDH/M |
| GSN (gelsolin (amyloidosis, Finnish type))             | X04412   | Hs.290070 | NM_000177 | 9q33         | Cluster Incl. X04412:Human mRNA for plasma gelsolin /cds=(14,2362) /gb=X04412 /gi=35447 /ug=Hs.80562  | 32812_at        |

|  |          |           |           |       |  |  |            |
|--|----------|-----------|-----------|-------|--|--|------------|
|  |          |           |           |       |  | /len=2602  |            |
| GATA2 (GATA-binding protein 2)   | M77810   | Hs.334695 | NM_002050 | 3q21  |  | M77810<br>/DEFINITION=HUMGATA2A Human<br>transcription factor GATA-2 (GATA-2)<br>mRNA, complete cds  | 1072_g_at  |
| HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)) | L24521   | Hs.89525  | NM_004494 | Xq25  |  | Cluster Incl. L24521:Human<br>transformation-related protein mRNA, 3<br>end /cds=(0,1108) /gb=L24521 /gi=403459<br>/ug=Hs.169225 /len=1240 | 38446_s_at |
| TUBG1 (tubulin, gamma 1)   | M61764   | Hs.21635  | NM_001070 | 17q21 |  | Cluster Incl. M61764:Human gamma-<br>tubulin mRNA, complete cds<br>/cds=(24,1379) /gb=M61764 /gi=183702<br>/ug=Hs.21635 /len=1568          | 33346_r_at |
| NUDEL(nuclear distribution gene E-like)                                    | AF038203 | Hs.3850   | NM_030808 | 17    |  | Cluster Incl. AF038203:Homo sapiens<br>clone 23596 mRNA sequence<br>/cds=UNKNOWN /gb=AF038203<br>/gi=2795924 /ug=Hs.3850 /len=1473         | 34413_at   |

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|---|----------|-----------|-----------|----------|---|------------------|
| TYMS (thymidylate synthetase)                         | D00596   | Hs.82962  | NM_001071 | 18p11.32 | D00596<br>/DEFINITION=HUMTS1 Homo sapiens<br>gene for thymidylate synthase, exons 1, 2,<br>3, 4, 5, 6, 7, complete cds  | 1505_at          |
| GAPD<br>(glyceraldehyde-3-phosphate<br>dehydrogenase) | M33197   | Hs.169476 | NM_002046 | 12p13    | Homo sapiens<br>/DEF=Human glyceraldehyde-3-phosphate<br>dehydrogenase (GAPDH) mRNA,<br>complete cds /LEN=1268 (5' _M, _3<br>represent transcript regions 5 prime,<br>Middle, and 3 prime respectively) | AFFX-HUMGAP.B1/M |
| EZH2 (enhancer of zeste (Drosophila) homolog<br>2)    | U61145   | Hs.77256  | NM_004456 | 7q35-q36 | Cluster Incl. U61145:Human enhancer of<br>zeste homolog 2 (EZH2) mRNA, complete<br>cds /cds=(89,2329) /gb=U61145<br>/gi=1575348 /ug=Hs.77256 /len=2600  | 37305_at         |
| STK12 (serine/threonine kinase 12)                    | AF015254 | Hs.180655 | NM_004217 | 17p13.1  | Cluster Incl. AF015254:Homo sapiens<br>serine/threonine kinase (STK-1) mRNA,<br>complete cds /cds=(58,1101)<br>/gb=AF015254 /gi=4090840   | 33266_at         |

|  |          |           |           |               |   |  |            |  |
|--|----------|-----------|-----------|---------------|---|--|------------|--|
|  |          |           |           |               |   | /ug=Hs.180655 /len=1234  |            |  |
| MPB1 (MYC promoter-binding protein 1)  | M55914   | Hs.284127 | NM_005945 | 1pter-p35     | M55914  | /FEATURE=<br>/DEFINITION=HUMCMYCQ Human c-myc<br>binding protein (MBP-1) mRNA, complete<br>cds | 2035_s_at  |  |
| PTTG1 (pituitary tumor-transforming 1) | AA203476 | Hs.252587 | NM_004219 | 5q35.1        | Cluster Incl. AA203476:zx55e01.r1 Homo<br>sapiens cDNA, 5 end /clone=IMAGE-<br>446424 /clone_end=5 /gb=AA203476<br>/gi=1799203 /ug=Hs.159626 /len=828 |  | 40412_at   |  |
| ICA1 (islet cell autoantigen 1 (69kD)) | U38260   | Hs.167927 | NM_004968 | 7p22          | Cluster Incl. U38260:Human Islet cell<br>autoantigen ICAp69 mRNA, complete cds<br>/cds=(169,942) /gb=U38260 /gi=1675205<br>/ug=Hs.167927 /len=1415    |  | 32634_s_at |  |
| PGD (phosphogluconate dehydrogenase)   | U30255   | Hs.75888  | NM_002631 | 1p36.3-p36.13 | Cluster Incl. U30255:Human<br>phosphogluconate dehydrogenase<br>(hPGDH) gene, complete cds<br>/cds=(6,1457) /gb=U30255 /gi=984324                     |  | 36963_at   |  |

|  |          |          |           |              |  |  |          |
|--|----------|----------|-----------|--------------|--|--|----------|
|  |          |          |           |              |  | /ug=Hs.75888 /len=1536   |          |
| FOXM1 (forkhead box M1)                            | U74612   | Hs.239   | NM_021953 | 12p13        |  | Cluster Incl. U74612:Human hepatocyte nuclear factor-3/fork head homolog 11A (HFN-11A) mRNA complete cds /cds=(114,2519) /gb=U74612 /gi=1842252 /ug=Hs.239 /len=3474 | 34715_at |
| BPI (bactericidal/permeability-increasing protein) | J04739   | Hs.89535 | NM_001725 | 20q11.23-q12 |  | Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535 /len=1813         | 37054_at |
| H2AFY (H2A histone family, member Y)               | AF054174 | Hs.75258 | NM_004893 | 5q31.3-q32   |  | Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete cds /cds=(173,1288) /gb=AF054174 /gi=3341991 /ug=Hs.75258 /len=1881                           | 36576_at |
| TKT (transketolase (Wernicke-Korsakoff syndrome))  | L12711   | Hs.89643 | NM_001064 | 3p14.3       |  | Cluster Incl. L12711:Homo sapiens transketolase (tk) mRNA, complete cds  | 38789_at |

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| syndrome))  |          |           |           |         |  | /cds=(98,1969) /gb=L12711 /gi=388890<br>/ug=Hs.89643 /len=2069  |          |  |  |  |
| GCDH (glutaryl-Coenzyme A dehydrogenase)                          | AD000092 | Hs.184141 | NM_000159 | 19p13.2 |  | AD000092 /FEATURE=cds#4<br>/DEFINITION=CH19HHR23 Homo sapiens<br>DNA from chromosome 19p13.2 cosmids<br>R31240, R30272 and R28549 containing<br>the EKL, GCDH, CRT, and RAD23A<br>genes, genomic sequence | 1749_at  |  |  |  |
| RAD54L (RAD54 (S.cerevisiae)-like)                                | X97795   | Hs.66718  | NM_003579 | 1p32    |  | X97795 /FEATURE=cds<br>/DEFINITION=HSRAD54 H.sapiens<br>mRNA homologous to S. cerevisiae<br>RAD54   | 966_at   |  |  |  |
| GNG5 (guanine nucleotide binding protein (G<br>protein), gamma 5) | AI541042 | Hs.5322   | NM_005274 | 1p22    |  | Cluster Incl. AI541042:pec1.2-1.D12.r<br>Homo sapiens cDNA, 5' end /clone_end=5<br>/gb=AI541042 /gi=4458415 /ug=Hs.5322<br>/len=688   | 35272_at |  |  |  |
| RAB32 (RAB32, member RAS oncogene family)                         | U59878   | Hs.32217  | NM_006834 | 6       |  | Cluster Incl. U59878:Human low-Mr GTP-<br>binding protein (RAB32) mRNA, partial cds   | 41523_at |  |  |  |



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|--|----------|----------|-----------|---------------|--|---|--|--|----------|
|  |          |          |           |               |  | /cds=(0,632) /gb=U59878 /gi=1388196<br>/ug=Hs.32217 /len=980  |  |  |          |
| CD63 (CD63 antigen (melanoma 1 antigen))   | X62654   | Hs.76294 | NM_001780 | 12q12-q13     |  | Cluster Incl. X62654:H.sapiens gene for<br>Me491/CD63 antigen /cds=(69,785)<br>/gb=X62654 /gi=430755 /ug=Hs.76294<br>/len=873   |  |  | 37003_at |
| MPO (myeloperoxidase)  | M19507   | Hs.1817  | NM_000250 | 17q23.1       |  | Cluster Incl. M19507:Human<br>myeloperoxidase mRNA, complete cds<br>/cds=UNKNOWN /gb=M19507 /gi=188657<br>/ug=Hs.1817 /len=3215 |  |  | 33284_at |
| TALDO1 (transaldolase 1)   | AF010400 | Hs.77290 | NM_006755 | 11p15.5-p15.4 |  | Cluster Incl. AF010400:untitled<br>/cds=(50,1063) /gb=AF010400<br>/gi=2612878 /ug=Hs.77290 /len=1242                            |  |  | 37311_at |
| CDKN3 (cyclin-dependent kinase inhibitor 3<br>(CDK2-associated dual specificity<br>phosphatase)) | L25876   | Hs.84113 | NM_005192 | 14q22         |  | L25876 /FEATURE=<br>/DEFINITION=HUMPTPB Homo sapiens<br>protein tyrosine phosphatase<br>(CIP2)mRNA, complete cds                |  |  | 1599_at  |

|  |          |           |           |             |   |          |
|--|----------|-----------|-----------|-------------|---|----------|
| H2AV( histone H2A.F/Z variant )                            | AW007731 | Hs.301005 | NM_012412 | 7           | Cluster Incl. AW007731:w68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512629 /clone_end=3 /gb=AW007731 /gi=5856509 /ug=Hs.9242 /len=659   | 39092_at |
| TXN (thioredoxin)  | AI653621 | Hs.76136  | NM_003329 | 9q31        | Cluster Incl. AI653621:t221b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2289213 /clone_end=3 /gb=AI653621 /gi=4737600 /ug=Hs.76136 /len=598 | 36992_at |
| ALAS1 (aminolevulinate, delta-, synthase 1)                | Y00451   | Hs.78712  | NM_000688 | 3p21.1      | Cluster Incl. Y00451:Human mRNA for 5-aminolevulinate synthase /cds=(83,2011) /gb=Y00451 /gi=36648 /ug=Hs.78712 /len=2156                   | 37674_at |
| NUCB2 (nucleobindin 2)                                     | X76732   | Hs.3164   | NM_005013 | 11p15.1-p14 | Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2708486 /ug=Hs.3164 /len=1586                           | 35643_at |
| BN51T (BN51 (BHK21) temperature sensitivity complementing) | M17754   | Hs.1276   | NM_001722 | 8q21        | Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754  | 41694_at |

|  |          |           |           |        |  |  |            |
|--|----------|-----------|-----------|--------|--|--|------------|
| complementing)   |          |           |           |        |  | /gi=179512 /ug=Hs.1276 /len=1881   |            |
| CCR2 (chemokine (C-C motif) receptor 2)                                    | U95626   | Hs.395    | NM_000647 | 3p21.1 |  | Cluster Incl. U95626: Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607 | 37149_s_at |
| DEFA4 (defensin, alpha 4, corticostatin)                                   | A1250799 | Hs.2582   | NM_001925 | 8p23   |  | Cluster Incl. A1250799: q136g07.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1858620 /clone_end=3 /gb=A1250799 /gi=3847328 /ug=Hs.2582 /len=542   | 34546_at   |
| HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)) | D16431   | Hs.89525  | NM_004494 | xq25   |  | Cluster Incl. D16431: Human mRNA for hepatoma-derived growth factor, complete cds /cds=(315,1037) /gb=D16431 /gi=598955 /ug=Hs.89525 /len=2376   | 38779_r_at |
| EPB72 (erythrocyte membrane protein band 7.2 (stomatlin))                  | X85116   | Hs.160483 | NM_004099 | 9q34.1 |  | Cluster Incl. X85116: H. sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035  | 40419_at   |

|   |        |           |           |             |  |   |                 |  |
|---|--------|-----------|-----------|-------------|--|---|-----------------|--|
|   |        |           |           |             |  | /gi=1161561 /ug=Hs.160483 /len=3035   |                 |  |
| DEFA3 (defensin, alpha 3, neutrophil-specific)  | L12691 | Hs.294176 | NM_005217 | 8pter-p23.3 |  | Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452   | 31508_s_at      |  |
| ACTG1 (actin, gamma 1)                          | X04098 | Hs.14376  | NM_001614 | 17q25       |  | Cluster Incl. X04098:Human mRNA for cytoskeletal gamma-actin /cds=(73,1200) /gb=X04098 /gi=28338 /ug=Hs.234733 /len=1918  | 34160_at        |  |
| GAPD (glyceraldehyde-3-phosphate dehydrogenase) | M33197 | Hs.169476 | NM_002046 | 12p13       |  | Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively) | AFFX-HUNGAPDH/M |  |
| KIAA0008( KIAA0008 gene product )               | D13633 | Hs.77695  | NM_014750 | 14          |  | Cluster Incl. D13633:Human mRNA for KIAA0008 gene, complete cds /cds=(121,2418) /gb=D13633 /gi=286012   | 37231_at        |  |

|  |  |         |           |  |           |                        |   |  |            |  |
|--|--|---------|-----------|--|-----------|------------------------|---|--|------------|--|
|  |  |         |           |  |           | /ug=Hs.77695 /len=2640 |   |  |            |  |
| LDHA (lactate dehydrogenase A)   |  | X02152: | Hs.2795   |  | NM_005566 | 11p15.4                | Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) /cds=(97,1095) /gb=X02152 /gi=34312 /ug=Hs.2795 /len=1661  |  | 41485_at   |  |
| ACTN1 (actinin, alpha 1)   |  | M95178  | Hs.119000 |  | NM_001102 | 14q24                  | Cluster Incl. M95178:Human non-muscle alpha-actinin mRNA, complete cds /cds=(111,2789) /gb=M95178 /gi=178051 /ug=Hs.119000 /len=3081        |  | 39330_s_at |  |
| PRG2 (proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic |  | Z26248  | Hs.99962  |  | NM_002728 | 11q12                  | Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=840510 /ug=Hs.99962 /len=1637 |  | 39179_at   |  |
| TCN1 (transcobalamin I (vitamin B12 binding protein, R binder family))                           |  | J05068  | Hs.2012   |  | NM_001062 | 11q11-q12              | Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75,1376) /gb=J05068 /gi=307478 /ug=Hs.2012 /len=1537                   |  | 35919_at   |  |

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|---|----------|-----------|-----------|---------------|--|--------------------|
| GGH (gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase)) | U55206   | Hs.78619  | NM_003878 | : 8p22-q21.13 | Cluster Incl. U55206: Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds /cds=(59,1015) /gb=U55206 /gi=2957143 /lug=Hs.78619 /len=1265 | 37263_at           |
| ACTB (actin, beta)  | X00351   | Hs.288061 | NM_001101 | 7p15-p12      | Homo sapiens mRNA -for beta-actin /DEF=Human /LEN=1761 /_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)               | AFFX-HSAC07/X00351 |
| LCN2 (lipocalin 2 (oncogene 24p3))  | A1762213 | Hs.204238 | NM_005564 | 9q34          | Cluster Incl. A1762213: wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=A1762213 /gi=5177880 /lug=Hs.204238 /len=677           | 32821_at           |
| AGPS (alkylglycerone phosphate synthase)                                    | Y09443   | Hs.22580  | NM_003659 | 2q31          | Cluster Incl. Y09443: H.sapiens mRNA for alkyl-dihydroxyacetonephosphate synthase precursor /cds=(15,1991) /gb=Y09443 /gi=1922284 /lug=Hs.22580          | 39225_at           |

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|--|----------|-----------|-----------|----------|--|-----------|--|--|
|  |          |           |           |          |  | /len=2074 |  |  |
| H2AFZ (H2A histone family, member Z)   | M37583   | Hs.119192 | NM_002106 | 4q24     | Cluster Incl. M37583:Human histone (H2A.Z) mRNA, complete cds /cds=(106,492) /gb=M37583 /gi=184059 /ug=Hs.119192 /len=873  | 39337_at  |  |  |
| MGC1780( hypothetical protein MGC1780 )  | AA926959 | Hs.77550  | NM_032636 | 1        | Cluster Incl. AA926959:om68h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1552383 /clone_end=3 /gb=AA926959 /gi=3075856 /ug=Hs.77550 /len=809                              | 37347_at  |  |  |
| CAT (catalase)   | AL035079 | Hs.76359  | NM_001752 | 11p13    | Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079 /gi=4775614 /ug=Hs.76359 /len=2287   | 37009_at  |  |  |
| SLC6A7 (solute carrier family 6 (neurotransmitter transporter, L-proline), member 7) | S80071   | Hs.241597 | NM_014228 | 5q31-q32 | Cluster Incl. S80071:hPROT=brain-specific L-proline transporter [human, hippocampus, mRNA Partial, 1911 nt] /cds=(0,1910) /gb=S80071 /gi=1839289 /ug=Hs.234765 /len=1911 | 34166_at  |  |  |

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|---|----------|-----------|-----------|----------|---|----------|
| TYMS (thymidylate synthetase)   | X02308   | Hs.82962  | NM_001071 | 18p11.32 | Cluster Incl. X02308:Human mRNA for thymidylate synthase (EC 2.1.1.45) /cds=(105,1046) /gb=X02308 /gi=37478 /ug=Hs.82962 /len=1536                                  | 37899_at |
| C20orf1 (chromosome 20 open reading frame 1)  | AB024704 | Hs.9329   | NM_012112 | 20q11.2  | Cluster Incl. AB024704:Homo sapiens mRNA for fis353, complete cds /cds=(471,2714) - /gb=AB024704 /gi=4589928 /ug=Hs.9329 /len=3403                                  | 39109_at |
| SERPINB1 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1) | M93056   | Hs.183583 | NM_030666 | 6p25     | Cluster Incl. M93056:Human monocyte/neutrophil elastase inhibitor mRNA sequence /cds=UNKNOWN /gb=M93056 /gi=188621 /ug=Hs.183583 /len=1298                          | 33305_at |
| DEEPEST( mitotic spindle coiled-coil related protein                                | AF063308 | Hs.16244  | NM_008461 | 17       | Cluster Incl. AF063308:Homo sapiens coiled-coil related protein DEEPEST (DEEPEST) mRNA, complete cds /cds=(69,3431) /gb=AF063308 /gi=4106355 /ug=Hs.16244 /len=3770 | 32120_at |



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|---|--------|-----------|-----------|--------------|---|----------|
| SLPI (secretory leukocyte protease inhibitor<br>(antileukoprotease))                            | X04470 | Hs.251754 | NM_003064 | 20pter-p12.3 | Cluster Incl. X04470:Human mRNA for<br>antileukoprotease (ALP) from cervix uterus<br>/cds=(18,416) /gb=X04470 /gi=28638<br>/ug=Hs.169793 /len=594 | 32275_at |
| TTK (TTK protein kinase)  | M86699 | Hs.169840 | NM_003318 | 6q13-q21     | M86699 /FEATURE=<br>/DEFINITION=HUMTTK Human kinase<br>(TTK) mRNA, complete cds   | 572_at   |
| ANXA1 (annexin A1)  | X05908 | Hs.78225  | NM_000700 | 9q12-q21.2   | Cluster Incl. X05908:Human mRNA for<br>lipocortin /cds=(74,1114) /gb=X05908<br>/gi=34387 /ug=Hs.78225 /len=1399                                   | 37403_at |
| CTSG (cathepsin G)  | M16117 | Hs.100764 | NM_001911 | 14q11.2      | Cluster Incl. M16117:Human cathepsin G<br>mRNA, complete cds /cds=(8,775)<br>/gb=M16117 /gi=181181 /ug=Hs.100764<br>/len=857                      | 37105_at |
| MS4A3 (membrane-spanning 4-domains,<br>subfamily A, member 3 (hematopoietic cell-<br>specific)) | L35848 | Hs.99960  | NM_006138 | 11q12-q13.1  | Cluster Incl. :Homo sapiens IgE receptor<br>beta chain (HTm4) mRNA, complete cds<br>/cds=UNKNOWN /gb=L35848 /gi=561638<br>/ug=Hs.99960 /len=1646  | 32451_at |

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|   |          |           |           |              |  | /lug=Hs.99960 /len=1646   |           |
| MGST2 (microsomal glutathione S-transferase 2)          | U77604   | Hs.81874  | NM_002413 | 4q28-q31     |  | U77604<br>/FEATURE=<br>/DEFINITION=HSU77604 Homo sapiens<br>microsomal glutathione S-transferase 2<br>(MGST2) mRNA, complete cds  | 820_at    |
| CLC (Charot-Leyden crystal protein)                     | L01664   | Hs.132004 | NM_013246 | 11q13.3      |  | Cluster Incl. L01664:Human eosinophil<br>Charot-Leyden crystal (CLC) protein<br>(lysophospholipase) mRNA, complete cds<br>/cds=(33,461) /gb=L01664 /gi=187273<br>/lug=Hs.889 /len=586 | 36809_at  |
| FLJ10140( hypothetical protein FLJ10140 )               | AL031588 | Hs.250671 | NM_018006 | 22           |  | Cluster Incl. AL031588:dJ1163J1.3 (novel<br>protein similar to mouse B99)<br>/cds=(0,2140) /gb=AL031588 /gi=4007108<br>/lug=Hs.122552 /len=2821                                       | 39872_at  |
| GADD45A (growth arrest and DNA-damage-inducible, alpha) | M60974   | Hs.80409  | NM_001924 | 1p31.2-p31.1 |  | M60974<br>/FEATURE=<br>/DEFINITION=HUMGADD45 Human<br>growth arrest and DNA-damage-inducible  | 1911_s_at |

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|---|----------|-----------|-----------|---------|--|--|----------|
|   |          |           |           |         |  | protein (gadd45) mRNA, complete cds  |          |
| OAT (ornithine aminotransferase (gyrate atrophy))                   | M12267   | Hs.75485  | NM_000274 | 10q26   |  | Cluster Incl. M12267:Human ornithine aminotransferase mRNA, complete cds /cds=(54,1373) /gb=M12267 /gi=189328 /ug=Hs.75485 /len=2013             | 36636_at |
| CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8) | M33326   | Hs.41     | NM_001816 | 19q13.2 |  | Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287  | 33530_at |
| S100A8 (S100 calcium-binding protein A8 (calgranulin A))            | A1126134 | Hs.100000 | NM_002984 | 1q21    |  | Cluster Incl. A1126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=A1126134 /gi=3594648 /ug=Hs.100000 /len=446     | 41096_at |
| U67369  | U67369   | Hs.73172  | NM_005263 | 1p22    |  | Cluster Incl. U67369:Human growth factor independence-1 (Gfi-1) mRNA, complete cds /cds=(267,1535) /gb=U67369 /gi=1698691 /ug=Hs.73172 /len=2799 | 33977_at |

| TFDP2 (transcription factor Dp-2 (E2F dimerization partner 2))                                | L40386 | Hs.19131  | NM_006286 | 3q23    | L40386<br>/DEFINITION=HUMDP2M Human DP-2 mRNA, complete cds   | 633_s_at   |
|---|--------|-----------|-----------|---------|---|------------|
| ELA2 (elastase 2, neutrophil)   | M34379 | Hs.99863  | NM_001972 | 19p13.3 | Cluster Incl. M34379:Human elastase/medullasin mRNA, complete cds /cds=(38,841) /gb=M34379 /gi=187116 /ug=Hs.99863 /len=920 -                               | 37096_at   |
| ITGAM (integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), | J03925 | Hs.172631 | NM_000632 | 16p11.2 | Cluster Incl. J03925:Human Mac-1 gene encoding complement receptor type 3, CD11b, complete cds /cds=(72,3533) /gb=J03925 /gi=187284 /ug=Hs.172631 /len=4699 | 38533_s_at |
| AZU1 (azurocidin 1 (cationic antimicrobial protein 37))                                       | M96326 | Hs.72885  | NM_001700 | 19p13.3 | Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771) /gb=M96326 /gi=179301 /ug=Hs.72885 /len=913  | 33963_at   |

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|--|--------|-----------|-----------|-------|---|------------|
| PKM2 (pyruvate kinase, muscle)                           | M26252 | Hs.198281 | NM_002654 | 15q22 | Cluster Incl. M26252:Human thyroid hormone-binding protein, complete cds<br>/cds=(89,1894) /gb=M26252 /gi=338826 /ug=Hs.198281 /len=2308                              | 32378_at   |
| S100A9 (S100 calcium-binding protein A9 (calgranulin B)) | W72424 | Hs.112405 | NM_002965 | 1q21  | Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604                              | 41471_at   |
| CKS2 (CDC28 protein kinase 2)                            | X54942 | Hs.83758  | NM_001827 | 9q22  | Cluster Incl. X54942:H.sapiens cks2 mRNA for Cks1 protein homologue<br>/cds=(95,334) /gb=X54942 /gi=29978 /ug=Hs.83758 /len=612                                       | 40690_at   |
| GAPD (glyceraldehyde-3-phosphate dehydrogenase)          | U34995 | Hs.169476 | NM_002046 | 12p13 | Cluster Incl. U34995:Human normal keratinocyte subtraction library mRNA, clone H22a, complete sequence<br>/cds=UNKNOWN /gb=U34995 /gi=1497857 /ug=Hs.195188 /len=1626 | 35905_s_at |

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| LOC95295( hypothetical gene supported by<br>V00599; BC001938; BC007605; BC008791 | V00599   |           |           |          | 6 | V00599<br>/DEFINITION=HSTUB2 Human mRNA<br>fragment encoding beta-tubulin. (from<br>clone D-beta-1)                                     | 151_s_at |
| ADAM15 (a disintegrin and metalloproteinase<br>domain 15 (metargidin))           | U41767   | Hs.92208  | NM_003815 | 1q21.3   |   | Cluster Incl. U41767:Human metargidin<br>precursor mRNA, complete cds<br>/cds=(7,2451) /gb=U41767 /gj=1235673<br>/ug=Hs.92208 /len=2725 | 38282_at |
| LOC51304( DHHC1 protein )  | AF052182 | Hs.14896  | NM_016598 | 3        |   | Cluster Incl. AF052182:Homo sapiens<br>clone 24590 mRNA sequence<br>/cds=UNKNOWN /gb=AF052182<br>/gj=3360494 /ug=Hs.14896 /len=1298     | 39751_at |
| RAB13 (RAB13, member RAS oncogene family)  | X75593   | Hs.151536 | NM_002870 | 12q13    |   | Cluster Incl. X75593:H.sapiens mRNA for<br>rab 13 /cds=(139,750) /gb=X75593<br>/gj=452319 /ug=Hs.151536 /len=1238                       | 40210_at |
| BZRP (benzodiazepine receptor (peripheral))                                      | M36035   | Hs.202    | NM_000714 | 22q13.31 |   | Cluster Incl. M36035:Human peripheral<br>benzodiazepine receptor (hpbs) mRNA,<br>complete cds /cds=(61,570) /gb=M36035                  | 32806_at |

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|---|--------|-----------|-----------|------|--|---|----------|
|   |        |           |           |      |  | /gi=184333 /ug=Hs.202 /len=811  |          |
| KNXL6 (kinesin-like 6 (mitotic centromere-associated kinesin))  | U63743 | Hs.69360  | NM_006845 | 1    |  | Cluster Incl. U63743:Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds /cds=(54,2231) /gb=U63743 /gi=1695881 /ug=Hs.69360 /len=2740 | 36837_at |
| MTX1 (metaxin 1)  | U46920 | Hs.247551 | NM_002455 | 1q21 |  | Cluster Incl. U46920:Human metaxin (MTX) gene, complete cds /cds=(0,953) /gb=U46920 /gi=1326107 /ug=Hs.181246 /len=1065                                 | 40890_at |
| DOK1 (docking protein 1, 62kD (downstream of tyrosine kinase 1) | U70987 | Hs.103854 | NM_001381 | 2p13 |  | U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein p62dok (DOK) mRNA, complete cds   | 816_g_at |
| E2-EPF( ubiquitin carrier protein )                             | M91670 |           |           | 17   |  | M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds   | 893_at   |

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| NCF4 (neutrophil cytosolic factor 4 (40kD)) | AL008637 | Hs.196352 | NM_000631 | 22q13.1 | Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 - /gi=3136000 /lug=Hs.196352 /len=1744 | 38894_g_at |
| PGK1 (phosphoglycerate kinase 1)            | V00572   | Hs.78771  | NM_000291 | xq13    | Cluster Incl. V00572:Human mRNA encoding phosphoglycerate kinase /cds=(79,1332) /gb=V00572 /gi=35434 /lug=Hs.78771 /len=1767   | 37677_at   |
| S100P (S100 calcium-binding protein P)      | AA131149 | Hs.2962   | NM_005980 | 4p16    | Cluster Incl. AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-587049 /clone_end=5 /gb=AA131149 /gi=1692640 /lug=Hs.2962 /len=464   | 34319_at   |



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| NKG7 (natural killer cell group 7 sequence)  | S69115 | Hs.10306  | NM_005601 | 19q13.4   | Cluster Incl. S69115:granulocyte colony-stimulating factor induced gene [human, CML patient, bone marrow mononuclear cells, mRNA, 833 nt] /cds=(180,677) /gb=S69115 /gi=545708 /ug=Hs.10306 /len=833 | 37121_at |
| ITGA5 (integrin, alpha 5 (fibronectin receptor, alpha polypeptide)                     | X06256 | Hs.149609 | NM_002265 | 12q11-q13 | Cluster Incl. X06256:Human mRNA for integrin alpha 5 subunit /cds=(23,3172) /gb=X06256 /gi=31437 /ug=Hs.149609 /len=4204   | 39753_at |
| PKMYT1(membrane-associated tyrosine-and threonine-specific cdc2-inhibitory kinase      | U56816 | Hs.77783  | NM_004203 | 16        | U56816 /FEATURE= /DEFINITION=HSU56816 Human kinase Myt1 (Myt1) mRNA, complete cds  | 480_at   |
| CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross | M18728 | Hs.73848  | NM_002483 | 19q13.2   | Cluster Incl. M18728:Human nonspecific crossreading antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533   | 36105_at |

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| CREG (cellular repressor of E1A-stimulated genes)   | AF084523 | Hs.5710   | NM_003851 | 1q24          | Cluster Incl. AF084523:Homo sapiens cellular repressor of E1A-stimulated genes<br>CREG mRNA, complete cds /cds=(33,695)<br>/gb=AF084523 /gi=3550342 /ug=Hs.5710<br>/len=1974 | 35311_at |
| KIAA0374( syntrophin )  | AB002372 |           |           | 20            | Cluster Incl. AB002372:Human mRNA for KIAA0374 gene, complete cds<br>/cds=(642,2258) /gb=AB002372<br>/gi=2224688 /ug=Hs.100837 /len=5530                                     | 41107_at |
| MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase | J05070   | Hs.151738 | NM_004994 | 20q11.2-q13.1 | Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds<br>/cds=(19,2142) /gb=J05070 /gi=177204<br>/ug=Hs.151738 /len=2334   | 31859_at |
| CDW52 (CDW52 antigen (CAMPATH-1 antigen))   | N90866   | Hs.276770 | NM_001803 | 1p36          | Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-301723 /clone_end=3 /gb=N90866<br>/gi=1444193 /ug=Hs.214742 /len=577                                  | 34210_at |

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|---|----------|-----------|-----------|--------|---|-----------|
| TRB@ (T cell receptor beta locus)                                 | M12886   | Hs.303157 |           | 7q35   | M12886<br>/DEFINITION=HUMTCBY Human T-cell<br>receptor active beta-chain mRNA,<br>complete cds  | 1105_s_at |
| TAB2( TAK1-binding protein 2 )                                    | AB018276 | Hs.109727 | NM_015093 |        | Cluster Incl. AB018276:Homo sapiens<br>mRNA for KIAA0733 protein, partial cds<br>/cds=(0,1586) /gb=AB018276 /gi=3882186<br>/ug=Hs.109727 /len=3479          | 38980_at  |
| TNFRSF7 (tumor necrosis factor receptor<br>superfamily, member 7) | M63928   | Hs.180841 | NM_001242 | 12p13  | Cluster Incl. M63928:Homo sapiens T cell<br>activation antigen (CD27) mRNA,<br>complete cds /cds=(100,882) /gb=M63928<br>/gi=180084 /ug=Hs.180841 /len=1204 | 38578_at  |
| KIAA0275( KIAA0275 gene product )                                 | D87465   | Hs.74583  | NM_014767 |        | Cluster Incl. D87465:Human mRNA for<br>KIAA0275 gene, complete cds<br>/cds=(316,1590) /gb=D87465 /gi=1665814<br>/ug=Hs.74583 /len=5316                      | 36155_at  |
| PTCH (patched (Drosophila) homolog)                               | U59464   | Hs.159526 | NM_000264 | 9q22.3 | Cluster Incl. U59464:Human PATCHED<br>protein (PTC) mRNA, complete cds  | 38214_at  |

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|---|--------|----------|-----------|--|--------|--|--|--|--|--|----------|
|   |        |          |           |  |        | /cds=(0,4343) /gb=U59464 /gi=1381235<br>/ug=Hs.159526 /len=4344  |  |  |  |  |          |
| TRAM( translocating chain-associating membrane protein )          | X63679 | Hs.4147  | NM_014294 |  |        | Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /gb=X63679 /gi=37264 /ug=Hs.4147 /len=1267                             |  |  |  |  | 34796_at |
| HLA-DMA (major histocompatibility complex, class II, DM alpha)    | X62744 | Hs.77522 | NM_006120 |  | 6p21.3 | Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079    |  |  |  |  | 37344_at |
| HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1) | X00457 | Hs.914   |           |  | 6p21.3 | Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048 |  |  |  |  | 38833_at |
| KIAA1128( KIAA1128 protein )                                      | U90912 | Hs.81897 |           |  |        | Cluster Incl. U90912:Human clone 23865 mRNA sequence /cds=UNKNOWN /gb=U90912 /gi=1913892 /ug=Hs.81897  |  |  |  |  | 37617_at |

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|   |        |           |           |          |  | /len=1633   |  |  |  | 41723_s_at |
| HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)          | M32578 | Hs.180255 | NM_002124 | 6p21.3   |  | Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216                                  |  |  |  |            |
| MMD (monocyte to macrophage differentiation-associated)                   | X85750 | Hs.79889  | NM_012329 | 17q      |  | Cluster Incl. X85750:H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation /cds=(81,797) /gb=X85750 /gi=1008684 /ug=Hs.79889 /len=2518 |  |  |  | 37565_at   |
| HLA-DMB (major histocompatibility complex, class II, DM beta)             | U15085 | Hs.1162   | NM_002118 | 6p21.3   |  | Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362   |  |  |  | 41609_at   |
| TGFB3 (transforming growth factor, beta receptor III (betaglycan, 300kD)) | L07594 | Hs.75059  | NM_003243 | 1p33-p32 |  | L07594 /DEFINITION=HUMTGF3C Human transforming growth factor-beta type III  |  |  |  | 1897_at    |

|  |          |           |           |           |  | receptor (TGF-beta) mRNA, complete cds   |            |
|--|----------|-----------|-----------|-----------|--|--|------------|
| KRT10 (keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)) | X14487   | Hs.99936  | NM_000421 | 17q21-q23 |  | Cluster Incl. X14487:Human gene for acidic (type I) cytokeratin 10 /cds=(25,1806) /gb=X14487 /gi=28316 /ug=Hs.99936 /len=2166                | 38610_s_at |
| MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))                  | AB023208 | Hs.181002 | NM_006840 | 17q25     |  | Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938 | 41220_at   |
|  | A1700633 |           |           |           |  | Cluster Incl. A1700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343412 /clone_end=3 /gb=A1700633 /gi=4988533 /ug=Hs.4815 /len=565   | 34840_at   |
| CASP7 (caspase 7, apoptosis-related cysteine protease)                             | U67319   | Hs.9216   | NM_001227 | 10q25     |  | Cluster Incl. U67319:Human Lice2 beta cysteine protease mRNA, complete cds /cds=(228,1238) /gb=U67319 /gi=1894912 /ug=Hs.9216 /len=2602      | 38281_at   |

|  |          |          |           |        |  |            |
|--|----------|----------|-----------|--------|--|------------|
| SNRPN (small nuclear ribonucleoprotein polypeptide N)            | U41303   | Hs.48375 | NM_003097 | 15q12  | Cluster Incl. U41303:Human small nuclear ribonucleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326 | 34842_at   |
| HLA-DPB1 (major histocompatibility complex, class II, DP beta 1) | M83664   | Hs.814   | NM_002121 | 6p21.3 | Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501     | 38095_i_at |
| NCOA1 (nuclear receptor coactivator 1)                           | AJ000882 | Hs.74002 | NM_003743 | 2p23   | Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivator 1e /cds=(201,4400) /gb=AJ000882 /gi=2924310 /ug=Hs.74002 /len=4709                   | 36118_at   |
| HLA-DPB1 (major histocompatibility complex, class II, DP beta 1) | M83664   | Hs.814   | NM_002121 | 6p21.3 | Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814               | 38096_f_at |

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|---|----------|----------|-----------|---------------|--|---|----------|
|   |          |          |           |               |  | /len=1501   |          |
| PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytchesin 1))                | M85169   | Hs.1050  | NM_004762 | 17q25         |  | Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301            | 38666_at |
| KIAA1041( KIAA1041 protein )  | AB028964 | Hs.26023 | NM_014947 |               |  | Cluster Incl. AB028964:Homo sapiens mRNA for KIAA1041 protein, complete cds /cds=(312,2180) /gb=AB028964 /gi=5689418 /ug=Hs.26023 /len=5341 | 35163_at |
| SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6) | D87432   | Hs.10315 | NM_003983 | 16q22.1-q22.3 |  | Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1808) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296               | 39533_at |
|   | AF038199 |          |           |               |  | Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence /cds=UNKNOWN /gb=AF038199   | 38154_at |



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|--|----------|----------|-----------|--------|--|---|--|------------|--|
|  |          |          |           |        |  | /gi=2795920 /ug=Hs.153106 /len=1112   |  |            |  |
| UCP2 (uncoupling protein 2 (mitochondrial, proton carrier))      | U94592   | Hs.80658 | NM_003355 | 11q13  |  | Cluster Incl. U94592:Human uncoupling protein homolog (UCPH) mRNA, complete cds /cds=(314,1243) /gb=U94592 /gi=2052354 /ug=Hs.80658 /len=1888 |  | 37591_at   |  |
| HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1) | M81141   | Hs.73931 | NM_002123 | 6p21.3 |  | Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171  |  | 36773_f_at |  |
| NCOA1 (nuclear receptor coactivator 1)                           | U59302   | Hs.74002 | NM_003743 | 2p23   |  | U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds   |  | 484_at     |  |
| KIAA0542( KIAA0542 gene product )                                | AB011114 | Hs.62209 |           |        |  | Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, complete cds /cds=(393,3299) /gb=AB011114 /gi=3043607 /ug=Hs.62209 /len=5280   |  | 36545_s_at |  |

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|---|----------|-----------|-----------|--------------|---|----------------|
| JAK1 (Janus kinase 1 (a protein tyrosine kinase)) | AL039831 | Hs.50651  | NM_002227 | 1p32.3-p31.3 | Cluster<br>AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651 /len=579      | Incl. 34877_at |
| IGHM (immunoglobulin heavy constant mu)           | X67301   | Hs.302063 |           | 14q32.33     | Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453           | 41164_at       |
| DKFZP434C171( DKFZP434C171 protein                | AL080169 | Hs.209100 | NM_015621 |              | Cluster Incl. AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171) /cds=(0,544) /gb=AL080169 /gi=5262637 /ug=Hs.209100 /len=2595 | 34183_at       |
|   | X6730    |           |           |              | Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407                                   | 41165_g_at     |

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|--|----------|-----------|------------|-----------|--|--|------------|--|
|  |          |           |            |           |  | /ug=Hs.179543 /len=1453  |            |  |
| TMSB10 (thymosin, beta 10)               | M92383   | Hs.76293  | NIM_021103 | 2         |  | Cluster Incl. M92383:Homo sapiens thymosin beta-10 gene, 3end /cds=(0,149) /gb=M92383 /gi=339696 /ug=Hs.169250 /len=400                      | 31481_s_at |  |
| AHNAK (AHNAK nucleoprotein (desmoyokin)) | M80899   | Hs.301417 |            | 11q12-q13 |  | Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899 /gi=178282 /ug=Hs.76549 /len=4051             | 37027_at   |  |
| KIAA1002( KIAA1002 protein )             | AB023219 | Hs.20340  |            |           |  | Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete cds /cds=(800,3322) /gb=AB023219 /gi=4589647 /ug=Hs.102483 /len=4331 | 41366_at   |  |
| HBOA( histone acetyltransferase )        | AI951946 | Hs.21907  | NIM_007067 |           |  | Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523    | 41338_at   |  |

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|---|----------|-----------|-----------|----------|---|----------|
| RNF6 (ring finger protein (C3H2C3 type) 6)                                      | AJ010346 | Hs.32597  | NM_005977 | 13q12.2  | Cluster Incl. AJ010346:Homo sapiens mRNA for RING-H2 protein RNF6, alternative exon 1a /cds=(360,2417) /gb=AJ010346 /gi=4583651 /ug=Hs.32597 /len=3503              | 35656_at |
| IGHM (immunoglobulin heavy constant mu)   | X58529   | Hs.302063 |           | 14q32.33 | Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325 | 41166_at |
| KIAA0660(ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2) | AB014560 | Hs.6727   | NM_012297 |          | Cluster Incl. AB014560:Homo sapiens mRNA for KIAA0660 protein, complete cds /cds=(120,1568) /gb=AB014560 /gi=3327133 /ug=Hs.6727 /len=4210                          | 35793_at |
| KIAA1093( KIAA1093 protein )  | AB029016 | Hs.117333 |           |          | Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial cds /cds=(0,3613) /gb=AB029016 /gi=5689522 /ug=Hs.117333 /len=4159                           | 37487_at |

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|---|----------|-----------|-----------|--------------|--|----------|
| PRKRIR (protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, | AL049970 | Hs.177574 | NM_004705 | 11q13.5      | Cluster Incl. AL049970:Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102) /cds=(0,965) /gb=AL049970 /gi=4884219 /ug=Hs.177574 /len=2724  | 41141_at |
| SCAP1 (src family associated phosphoprotein 1)  | Y11215   | Hs.19126  | NM_003726 | 17q21.3      | Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524   | 38862_at |
| FLJ10140( hypothetical protein FLJ10140 )   | AL031588 | Hs.250671 | NM_018006 |              | Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438 | 41660_at |
| UBE2D2 (ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5))              | A1310002 | Hs.108332 | NM_003339 | 5p14.2-q23.3 | Cluster Incl. A1310002:qp77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=A1310002  | 38705_at |

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|  |          |           |  |  |           | /gi=4004873 /ug=Hs.108332 /len=656   |          |
| KIAA0226( KIAA0226 gene product )                                | D86979   | Hs.141296 |  |  |           | Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(622,2877) /gb=D86979 /gi=1504031 /ug=Hs.141296 /len=5891   | 31802_at |
| SEP2(sepin 6)  | D50918   | Hs.90998  |  |  | Hs.90998  | Cluster Incl. D50918:Human mRNA for KIAA0128 gene, partial cds /cds=(0,1276) /gb=D50918 /gi=1469178 /ug=Hs.90998 /len=4612   | 38826_at |
| UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC | D83004   | Hs.75355  |  |  | NM_003348 | 12<br>Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds /cds=(63,521) /gb=D83004 /gi=1181557 /ug=Hs.75355 /len=1203 | 36604_at |
| PKD2 (polycystic kidney disease 2 (autosomal dominant))          | AL050147 | Hs.91146  |  |  | NM_016457 | 19q13.2<br>Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630)   | 38269_at |

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|   |          |           |           |               |  | /gb=AL050147 /gi=4884153 /ug=Hs.91146<br>/len=1837  |            |  |  |  |
| RUNX3 (runt-related transcription factor 3)                         | Z35278   | Hs.170019 | NM_004350 | 1p36          | Z35278   | /FEATURE=mRNA<br>/DEFINITION=HSAML1RN H.sapiens<br>PEBP2aC1 acute myeloid leukaemia<br>mRNA | 106_at     |  |  |  |
| RAGA( Ras-related GTP-binding protein )                             | U41654   | Hs.57304  | NM_006570 |               | Cluster Incl. U41654;Human adenovirus<br>protein E3-14.7k interacting protein 1 (FIP-<br>1) mRNA, complete cds /cds=(243,1184)<br>/gb=U41654 /gi=2058395 /ug=Hs.57304<br>/len=1610 |   | 35316_at   |  |  |  |
| PPP1CC (protein phosphatase 1, catalytic<br>subunit, gamma isoform) | X74008   | Hs.79081  | NM_002710 | 12q24.1-q24.2 | Homo sapiens<br>/DEF=Cluster Incl. H.sapiens mRNA for<br>protein phosphatase 1 gamma<br>/cds=(154,1125) /gb=<br>/gi=402777<br>/ug=Hs.79081 /len=2263 /LEN=2431                     |   | 37725_at   |  |  |  |
| H2BFL (H2B histone family, member L)                                | AI688098 | Hs.239884 | NM_003526 | 6p21.3        | Cluster Incl. AI688098;wc92f08.x1 Homo<br>sapiens cDNA, 3 end /clone=IMAGE-  |   | 33458_r_at |  |  |  |

|                              |          |           |           |      |   |   |  |
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|                              |          |           |           |      |   | 2326119 /clone_end=3 /gb=AI688098<br>/gi=4899392 /ug=Hs.239884 /len=576 |  |
| BIN1 (bridging integrator 1) | U68485   | Hs.193163 | NM_004305 | 2q14 | U68485 /FEATURE=459_s_at<br>/DEFINITION=HSU68485 Homo sapiens<br>bridging integrator protein-1 (BIN1) mRNA,<br>complete cds                           |   |  |
|                              | AI749193 |           |           |      | Cluster Incl. AI749193:at40a04.x1 Homo<br>sapiens cDNA, 3 end /clone=IMAGE-<br>2374494 /clone_end=3 /gb=AI749193<br>/gi=5127457 /ug=Hs.17639 /len=544 | 40623_at  |  |
| KIAA0911(calsyntenin 1)      | AB020718 | Hs.29665  | NM_014944 |      | Cluster Incl. AB020718:Homo sapiens<br>mRNA for KIAA0911 protein, complete cds<br>/cds=(793,3738) /gb=AB020718<br>/gi=4240310 /ug=Hs.29665 /len=5219  | 41498_at  |  |
|                              | M13560   |           |           |      | Cluster Incl. M13560:Human la-associated<br>invariant gamma-chain gene<br>/cds=(795,1493) /gb=M13560 /gi=184518                                       | 35016_at  |  |



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|--|----------|-----------|-----------|--------------|--|------------------------|----------|--|
|  |          |           |           |              |  | /ug=Hs.84298 /len=2080 |          |  |
| RE (arginine-glutamic acid dipeptide (RE) repeats) | AB007927 | Hs.194369 | NM_012102 | 1p36.1-p36.2 | Cluster Incl. AB007927:Homo sapiens mRNA for KIAA0458 protein, complete cds /cds=(155,3961) /gb=AB007927 /gi=3413877 /ug=Hs.194369 /len=6642 |                        | 32253_at |  |
| NIFU( nitrogen fixation cluster-like )             | U47101   | Hs.9908   |           |              | Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819              |                        | 39165_at |  |
| CD48 (CD48 antigen (B-cell membrane protein))      | M37766   | Hs.901    | NM_001778 | 1q21.3-q22   | Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058                  |                        | 38006_at |  |
| BIN1 (bridging integrator 1)                       | AF001383 | Hs.193163 | NM_004305 | 2q14         | Cluster Incl. AF001383:Homo sapiens amphiphysin II mRNA, complete cds /cds=(171,1619) /gb=AF001383 /gi=2199534 /ug=Hs.193163 /len=2115       |                        | 32238_at |  |

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|--|----------|-----------|-----------|-----------|---|------------|
| KIAA0239( KIAA0239 protein )                 | D87076   | Hs.9729   | NM_015288 |           | Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716) /gb=D87076 /gi=1510152 /ug=Hs.9729 /len=5630                                 | 38342_at   |
| CSK (c-src tyrosine kinase)                  | X59932   | Hs.77793  | NM_004383 | 15q23-q25 | X59932 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase -  | 1768_s_at  |
| RGS10 (regulator of G-protein signalling 10) | AF045229 | Hs.82280  | NM_002925 | 10q25     | Cluster Incl. AF045229:Homo sapiens regulator of G protein signalling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753 | 33121_g_at |
| RBL2 (retinoblastoma-like 2 (p130))          | X76061   | Hs.79362  | NM_005611 | 16q12.2   | Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835                                     | 32597_at   |
| ZFR(zinc finger RNA binding protein)         | A1743507 | Hs.173518 | NM_016107 |           | Cluster Incl. A1743507:w72a08.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-   | 40610_at   |

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|   |          |           |           |          |  | 2361106 /clone_end=3 /gb=A1743507 /gi=5111795 /ug=Hs.173518 /len=733  |           |
| SIT(SHP2 interacting transmembrane adaptor            | AJ010059 | Hs.88012  | NM_014450 |          |  | Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232                               | 40723_at  |
| PFTK1 (PFTAIR protein kinase 1                        | AB020641 | Hs.57856  | NM_012395 | 7q21-q22 |  | Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957 | 36502_at  |
| CDR2 (cerebellar degeneration-related protein (62kD)) | M63256   | Hs.75124  |           | 16p12.3  |  | Cluster Incl. M63256:Human major Yo paraneoplastic antigen (CDR2) mRNA, 3 end /cds=(0,1529) /gb=M63256 /gi=180186 /ug=Hs.75124 /len=2570    | 36190_at  |
| IFI16 (interferon, gamma-inducible protein 16)        | M63838   | Hs.155530 | NM_005531 | 1q22     |  | M63838 /FEATURE= /DEFINITION=HUMIF16A Human interferon-gamma induced protein (IFI 16) gene, complete cds                                    | 1456_s_at |

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|---|----------|-----------|-----------|-------------|--|------------|
| TCL1A (T-cell leukemia/lymphoma 1A)                   | X82240   | Hs.2484   | NM_021966 | 14q32.1     | Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312  | 39318_at   |
| NAF1(Nef-associated factor 1                          | AJ011896 | Hs.109281 | NM_006058 |             | Cluster Incl. AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta) /cds=(110,2017) /gb=AJ011896 /gi=3758820 /ug=Hs.109281 /len=2710  | 38970_s_at |
| CD37 (CD37 antigen)                                   | X14046   | Hs.153053 | NM_001774 | 19p13-q13.4 | Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125  | 31870_at   |
| PLCG1 (phospholipase C, gamma 1 (formerly subtype 148 | AL022394 | Hs.268177 | NM_002660 | 20q12-q13.1 | Cluster Incl. AL022394:dJ511B24.2 (1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 /cds=(68,3940) /gb=AL022394 /gi=3288442 /ug=Hs.317 | 34351_at   |

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|  |  |  |  |  |  | /len=5151   |          |
|  |  |  |  |  |  | Cluster Incl. AB018272:Homo sapiens mRNA for KIAA0729 protein, partial cds /cds=(0,3591) /gb=AB018272 /gi=3882178 /ug=Hs.180948 /len=4143 | 41218_at |
| BLK (B lymphoid tyrosine kinase)   |  |  |  |  |  | S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]                                     | 854_at   |
|  |  |  |  |  |  | Cluster Incl. H24861:y142e11.1 Homo sapiens cDNA, 5' end /clone=IMAGE-160940 /clone_end=5 /gb=H24861 /gi=893760 /ug=Hs.90145 /len=517     | 33168_at |
| NFATC1 (nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1) |  |  |  |  |  | Cluster Incl. U08015:Human NF-ATc1 mRNA, complete cds /cds=(239,2389) /gb=U08015 /gi=500631 /ug=Hs.96149                                  | 39143_at |

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|---|--------|-----------|-----------|----------|---|---|-----------|
|   |        |           |           |          |   | /len=2743   |           |
|   |        |           |           |          |   | Transcription Factor Oct-1a/1b, Alt. Splice 2, Oct-1b   | 1171_s_at |
| IFNAR2 (Interferon (alpha, beta and omega) receptor 2)  | L42243 | Hs.86958  | NM_000874 | 21q22.11 | L42243  | /FEATURE=cds#3<br>/DEFINITION=HUMIFNAM08 Homo sapiens (clone 51H8) alternatively spliced interferon receptor (IFNAR2) gene, exon 9 and complete cds s | 1568_s_at |
| CD79A (CD79A antigen (immunoglobulin-associated alpha)) | U05259 | Hs.79630  | NM_001783 | 19q13.2  | Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107 |   | 38017_at  |
| XPA (xeroderma pigmentosum, complementation group A)    | D14533 | Hs.192803 | NM_000380 | 9q22.3   | D14533  | /FEATURE=<br>/DEFINITION=HUMXPAC Human mRNA for XPAC protein  | 1307_at   |
| TLK1 (tousled-like kinase 1)                            | D50927 | Hs.18895  | NM_012290 | 8p22-p12 | Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927                   |   | 32219_at  |

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|--|----------|-----------|-----------|---------|--|---|------------|
|  |          |           |           |         |  | /gi=1489198 /ug=Hs.18895 /len=4454  |            |
| SSH3BP1 (spectrin SH3 domain binding protein<br>1) | AF001628 | Hs.24752  | NM_005470 | 10p11.2 |  | Cluster Incl. AF001628:Homo sapiens<br>interactor protein AbiBP4 (AbiBP4) mRNA,<br>complete cds /cds=(48,1403)<br>/gb=AF001628 /gi=4100618<br>/ug=Hs.204036 /len=2175 | 38924_s_at |
| KIAA0494( KIAA0494 gene product )                  | AB007963 | Hs.62515  | NM_014774 |         |  | Cluster Incl. AB007963:Homo sapiens<br>mRNA for KIAA0494 protein, complete cds<br>/cds=(377,2464) /gb=AB007963<br>/gi=3413937 /ug=Hs.62515 /len=5766                  | 41830_at   |
| KIAA0014( KIAA0014 gene product )                  | D25216   | Hs.155650 | NM_014865 |         |  | Cluster Incl. D25216:Human mRNA for<br>KIAA0014 gene, complete cds<br>/cds=(146,1627) /gb=D25216 /gi=434774<br>/ug=Hs.155650 /len=5323                                | 32062_at   |
|  | U92980   |           |           |         |  | Cluster Incl. U92980:Homo sapiens clone<br>DT1P1A10 mRNA, CAG repeat region<br>/cds=UNKNOWN /gb=U92980  | 33242_at   |

|   |          |           |           |         |  |   |           |
|---|----------|-----------|-----------|---------|--|---|-----------|
|   |          |           |           |         |  | /gi=2781388 /ug=Hs.178207 /len=1423   |           |
| CD19 (CD19 antigen)   | M28170   | Hs.96023  | NM_001770 | 16p11.2 | M28170   | /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds | 1096_g_at |
| M17S2 (membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen | D30756   | Hs.277721 | NM_005689 | 17q21.1 | Cluster Incl. D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(140,3040) /gb=D30756 /gi=488500 /ug=Hs.233745 /len=4654                          |   | 33444_at  |
| LRMP (lymphoid-restricted membrane protein)   | U10485   | Hs.40202  | NM_006152 | 12p12   | Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds /cds=(574,2241) /gb=U10485 /gi=505685 /ug=Hs.40202 /len=2417 |   | 35974_at  |
| FLJ20274( hypothetical protein FLJ20274 )   | AA442799 | Hs.268371 | NM_017736 |         | Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-758875 /clone_end=5 /gb=AA442799  |   | 40868_at  |



|  |  |          |           |           |               |  |          |
|--|--|----------|-----------|-----------|---------------|--|----------|
|  |  |          |           |           |               | /gi=2155474 /ug=Hs.173992 /len=512   |          |
| IL10RA (interleukin 10 receptor, alpha)                            |  | U00672   | Hs.327    | NM_001558 | 11q23         | Cluster Incl. C:Human interleukin-10 receptor mRNA, complete cds /cds=(61,1797) /gb=U00672 /gi=482802 /ug=Hs.327 /len=3632                                   | 35659_at |
| RNF4 (ring finger protein 4)                                       |  | AB000468 | Hs.66394  | NM_002938 | 4p16.3        | Cluster Incl. AB000468:Homo sapiens mRNA for zinc finger protein, complete cds, clone-RES4-26 /cds=(297,869) /gb=AB000468 /gi=1843400 /ug=Hs.66394 /len=2903 | 35777_at |
| FCGR2B (Fc fragment of IgG, low affinity IIb, receptor for (CD32)) |  | M28696   | Hs.278443 | NM_004001 | 1q23          | Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450 /len=1416   | 34663_at |
| CLPTM1 (cleft lip and palate associated transmembrane protein      |  | AF037339 | Hs.106671 | NM_001294 | 19q13.2-q13.3 | Cluster Incl. AF037339:Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds   | 41413_at |

|                                     |        |           |           |  |   |          |
|-------------------------------------|--------|-----------|-----------|--|---|----------|
|                                     |        |           |           |  | /cds=(15,2024) /gb=AF037339 /gi=4063032 /ug=Hs.106671 /len=2468   |          |
| SP140( nuclear body protein Sp140 ) | U36500 | Hs.309943 | NM_007237 |  | Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173663 /ug=Hs.85283 /len=3252 | 40700_at |

Table 13:

| UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol | GenBank Accession No. | UniGene Cluster | RefSeq    | Chromosomal Location | Description UniGene Build #95   | Gene Name  |
|---|-----------------------|-----------------|-----------|----------------------|---|------------|
| MYH11 (myosin, heavy polypeptide 11, smooth muscle)   | AF001548              | Hs.78344        | NM_002474 | 16p13.13-p13.12      | AF001548 /FEATURE=mRNA /DEFINITION=HUA001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence  | 767_at     |
| ARHGAP4 (Rho GTPase activating protein 4)             | X78817                | Hs.3109         | NM_001666 | xq28                 | Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gl=840785 /ug=Hs.3109 /len=3236   | 39649_at   |
| MYH11 (myosin, heavy polypeptide 11, smooth muscle)   | AF013570              | Hs.78344        | NM_002474 | 16p13.13-p13.12      | Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gl=2352944 /ug=Hs.78344 /len=2580 | 37407_s_at |

|  |          |           |           |          |  |            |
|--|----------|-----------|-----------|----------|--|------------|
| PBX3 (pre-B-cell leukemia transcription factor 3)        | X59841   | Hs.294101 | NM_006195 | 9q33-q34 | Cluster Incl. X59841:Human PBX3 mRNA<br>/cds=UNKNOWN /gb=X59841 /gi=35314<br>/ug=Hs.171680 /len=2581   | 32696_at   |
| CTSW (cathepsin W (lymphopain))                          | AF013611 | Hs.87450  | NM_001335 | 11q13.1  | Cluster Incl. AF013611: Homo sapiens<br>lymphopain mRNA, complete cds<br>/cds=(0,1130) /gb=AF013611 /gi=2582044<br>/ug=Hs.87450 /len=1131          | 40718_at   |
| CDW52 (CDW52 antigen (CAMPATH-1<br>antigen))             | N90866   | Hs.276770 | NM_001803 | 1p36     | Cluster Incl. N90866:zb1b10.s1 Homo<br>sapiens cDNA, 3' end /clone=IMAGE-<br>301723 /clone_end=3 /gb=N90866<br>/gi=1444193 /ug=Hs.214742 /len=577  | 34210_at   |
| KIAA0906( KIAA0906 protein )                             | AB020713 | Hs.56966  |           | 3        | Cluster Incl. AB020713: Homo sapiens<br>mRNA for KIAA0906 protein, partial cds<br>/cds=(0,2772) /gb=AB020713 /gi=4240300<br>/ug=Hs.56966 /len=4217 | 41812_s_at |
| AOE372( thioredoxin peroxidase (antioxidant<br>enzyme) ) | U25182   | Hs.83383  | NM_006406 | 11       | Cluster Incl. U25182: Human antioxidant<br>enzyme AOE37-2 mRNA, complete cds<br>/cds=(43,858) /gb=U25182 /gi=799380                                | 38435_at   |

|   |          |           |           |           |  |  |          |
|---|----------|-----------|-----------|-----------|--|--|----------|
|   |          |           |           |           |  | /ug=Hs.83383 /len=921  |          |
| KIAA0246( KIAA0246 protein ), Similar to Mouse notch 3                              | D87433   | Hs.301989 | NM_015136 | 3         |  | Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777   | 38487_at |
| HOXB2 (homeo box B2)  | X16665   | Hs.2733   | NM_002145 | 17q21-q22 |  | Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520  | 39610_at |
| PLXNB2 (plexin B2)  | AB002313 | Hs.3989   |           | 22q13.33  |  | Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252  | 34780_at |
| SERPINB6 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6) | S69272   | Hs.41072  | NM_004568 | 6p25      |  | Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072 | 34789_at |

|   |          |          |           |              |  |           |  |
|---|----------|----------|-----------|--------------|--|-----------|--|
|   |          |          |           |              |  | /len=1465 |  |
| EIF4EL3 (eukaryotic translation initiation factor 4E-like 3)                  | AF038957 | Hs.19122 | NM_004846 | 2q37.1       | Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961 | 32229_at  |  |
| PLCB2 (phospholipase C, beta 2)   | M95678   | Hs.994   | NM_004573 | 15q15        | M95678 /FEATURE= Homo sapiens phospholipase C-beta-2 mRNA, complete cds  | 210_at    |  |
| SELL (selectin L (lymphocyte adhesion molecule 1))                            | M25280   | Hs.82848 | NM_000655 | 1q23-q25     | M25280 /FEATURE= Human lymph node homing receptor mRNA, complete cds   | 245_at    |  |
| NDUFC1 (NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (8kD, KFY1)) | AA760866 | Hs.84549 | NM_002494 | 4q28.2-q31.1 | Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549                                       | 38485_at  |  |

|  |          |           |           |             |   |            |
|--|----------|-----------|-----------|-------------|---|------------|
|  |          |           |           |             | /len=553  |            |
| PIG6( proline oxidase homolog )                                | AF010310 | Hs.274550 |           |             | Cluster Incl. AF010310: Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888           | 34110_g_at |
| HLA-DRA (major histocompatibility complex, class II, DR alpha) | J00194   | Hs.76807  | NM_019111 | 6p21.3      | Cluster Incl. J00194: human hla-dr antigen alpha-chain mRNA & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199            | 37039_at   |
|  |          |           |           |             | Cluster Incl. M13560: Human le-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080                 | 35016_at   |
| POU4F1 (POU domain, class 4, transcription factor 1)           | L20433   | Hs.211588 | NM_006237 | 13q21.1-q22 | Cluster Incl. L20433: Human octamer-binding transcription factor 1 (OTF-1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588 | 35939_s_at |

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|   |          |           |           |               |   |            |  |  |
|---|----------|-----------|-----------|---------------|---|------------|--|--|
|   |          |           |           |               |   | /len=3824  |  |  |
| XBP1 (X-box binding protein 1)  | Z93930   | Hs.149923 | NM_005080 | 22q12.1       | Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs; GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802 | 39756_g_at |  |  |
| NDUF85 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDHI)) | AF047181 | Hs.19236  | NM_002492 | 3q25.1-q25.33 | Cluster Incl. AF047181: Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034   | 32232_at   |  |  |
|   |          |           |           |               | Cluster Incl. AF052169: Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169  | 38972_at   |  |  |



|  |  |          |           |           |             |  |          |
|--|--|----------|-----------|-----------|-------------|--|----------|
|  |  |          |           |           |             | /gi=3360480 /ug=Hs.109438 /len=1385  |          |
| TIP30( Tal-interacting protein (30kD)  |  | AF039103 | Hs.90753  | NM_006410 | 11          | Cluster Incl. AF039103:Homo sapiens Tal-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297 | 38824_at |
| HOXA9 (homeo box A9)                   |  | U41813   | Hs.127428 | NM_002142 | 7p15-p14    | Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411              | 37809_at |
| VCL (vinculin)                         |  | M33308   | Hs.75350  | NM_003373 | 10q22.1-q23 | Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102                                 | 36601_at |
| DUSP6 (dual specificity phosphatase 6) |  | AB013382 | Hs.180383 | NM_001946 | 12q22-q23   | Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390                  | 41193_at |

|   |          |           |           |       |  |          |
|---|----------|-----------|-----------|-------|--|----------|
| PIG8(eloposide induced 2.4 mRNA)                                | AF010313 | Hs.286027 | NM_004879 | 11    | Cluster Incl. AF010313:Homo sapiens PIG8 (PIG8) mRNA, complete cds /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165                                 | 38097_at |
| SNRPN (small nuclear ribonucleoprotein polypeptide N)           | U41303   | Hs.48375  | NM_003097 | 15q12 | Cluster Incl. U41303:Human small nuclear ribonucleoprotein particle N (SNRPN) mRNA, complete cds - /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326 | 34842_at |
| TBC1D1 (TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1) | AB029031 | Hs.278586 |           | 4     | Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576                         | 32506_at |
| STAT12(cytokine inducible SH2-containing protein 2)             | AF037989 | Hs.110776 | NM_003877 | 12    | Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032 /ug=Hs.110776 /len=1937             | 38994_at |

|   |          |           |           |            |  |          |
|---|----------|-----------|-----------|------------|--|----------|
| GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))                     | M63904   | Hs.73797  | NM_002068 | 19p13.3    | Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060  | 40365_at |
| BZRP (benzodiazepine receptor (peripheral))   | M36035   | Hs.202    | NM_000714 | 22q13.31   | Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035 /gi=184333 /ug=Hs.202 /len=811                            | 32806_at |
| NPR3 (natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)) | M59305   | Hs.123655 | NM_000908 | 5p14-p13   | Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651 /ug=Hs.123655 /len=2081 | 34519_at |
| AGRN (agrin)  | AF016903 | Hs.273330 |           | 1p36.3-p32 | Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032                                       | 33454_at |

|  |          |           |           |             |  |          |
|--|----------|-----------|-----------|-------------|--|----------|
| EPB41L2 (erythrocyte membrane protein band 4.1-like 2)   | AF027299 | Hs.7857   | NM_001431 | 6q23        | Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /cds=(44,3061) /gb=AF027299 /gi=2739095 /ug=Hs.7857 /len=4316             | 32585_at |
| S100A8 (S100 calcium-binding protein A8 (calgranulin A)) | A1126134 | Hs.100000 | NM_002964 | 1q21        | Cluster Incl. A1126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 - /gb=A1126134 /gi=3594648 /ug=Hs.100000 /len=446 | 41096_at |
| POU4F1 (POU domain, class 4, transcription factor 1)     | X64624   | Hs.211588 | NM_006237 | 13q21.1-q22 | Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492       | 35940_at |
| LAK-4P( expressed in activated T/LAK lymphocytes )       | AB002405 | Hs.16165  | NM_007267 | 17          | Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=(108,1149) /gb=AB002405 /gi=2760120 /ug=Hs.16165 /len=1376              | 32116_at |

|  |          |          |           |         |   |          |
|--|----------|----------|-----------|---------|---|----------|
| ITGB2 (Integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)) | M15395   | Hs.83968 | NM_000211 | 21q22.3 | Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381) /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776 | 37918_at |
| NAGA (N-acetylgalactosaminidase, alpha-)   | Z99716   | Hs.75372 | NM_000262 | 22q11   | Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4458457 /ug=Hs.75372 /len=3606                                 | 36607_at |
| KLF4 (Kruppel-like factor 4 (gut))   | U70863   | Hs.7934  | NM_004235 | 9q31    | Cluster Incl. U70863:Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915) /gb=U70863 /gi=1857160 /ug=Hs.236377 /len=1953        | 36214_at |
| SIPA1 (signal-induced proliferation-associated gene 1)   | AB005666 | Hs.7019  | NM_006747 | 11q13.3 | Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein, complete cds /cds=(296,3424) /gb=AB005666 /gi=2389008 /ug=Hs.7019                       | 36843_at |

|   |          |           |           |               |  |  |          |  |
|---|----------|-----------|-----------|---------------|--|--|----------|--|
|   |          |           |           |               |  | /len=3885  |          |  |
| SPC18(signal peptidase complex (18kD))            | AI357653 | Hs.9534   | NM_014300 | 15            |  | Cluster Incl. AI357653:qy15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2012084 /clone_end=3 /gb=AI357653 /gi=4109274 /ug=Hs.9534 /len=833 | 39139_at |  |
| KIAA0223( minor histocompatibility antigen HA-1 ) | D86976   | Hs.196914 |           | 19            |  | Cluster Incl. D86976:Human mRNA for KIAA0223 gene, partial cds /cds=(0,3498) /gb=D86976 /gi=1504025 /ug=Hs.196914 /len=4121                | 33748_at |  |
| CALR (calreticulin)                               | M84739   | Hs.16488  | NM_004343 | 19p13.3-p13.2 |  | Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937        | 32543_at |  |
| MGC2747( hypothetical protein MGC2747             | AL046940 | Hs.250723 | NM_024104 | 19            |  | Cluster Incl. AL046940:DKFZp586i0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586i0517 /clone_end=5   | 41273_at |  |

|   |             |          |          |           |          |   |
|---|-------------|----------|----------|-----------|----------|---|
|   |             |          |          |           |          |   |
| SDR1(retinal dehydrogenase/reductase 1)   | short-chain | AF061741 | Hs.17144 | NM_004753 | 1        | /gb=AL046940 /gi=5434999<br>/ug=Hs.231657 /len=695<br>Cluster Incl. AF061741: Homo sapiens retinal dehydrogenase/reductase retSDR1 mRNA, complete cds /cds=(54,962) /gb=AF061741 /gi=3450827 /ug=Hs.17144 /len=1401<br>40782_at |
| CBFA2T1 (core-binding factor, runt domain, alpha subunit 2, translocated to, 1; cyclin D-related) |             | D43638   | Hs.31551 | NM_004349 | 8q22     | Cluster Incl. D43638: Human mRNA for MTC8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460<br>35638_at   |
| CPA3 (carboxypeptidase A3 (mast cell))  |             | M73720   | Hs.646   | NM_001670 | 3q21-q25 | Cluster Incl. M73720: Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633<br>36749_at  |

|  |        |           |           |         |   |            |
|--|--------|-----------|-----------|---------|---|------------|
| XBP1 (X-box binding protein 1)                                   | Z93930 | Hs.149923 | NM_005080 | 22q12.1 | Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802 | 39755_at   |
| DEK (DEK oncogene (DNA binding))                                 | X64229 | Hs.110713 | NM_003472 | 6p23    | Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502 /ug=Hs.110713 /len=2699   | 38992_at   |
| PTGER2 (prostaglandin E receptor 2 (subtype EP2), 53kD)          | U19487 | Hs.2090   | NM_000956 | 14q22   | U19487 /FEATURE= Human /DEFINITION=HSU19487 prostaglandin E2 receptor mRNA, complete cds  | 828_at     |
| HLA-DPB1 (major histocompatibility complex, class II, DP beta 1) | M83664 | Hs.814    | NM_002121 | 6p21.3  | Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814  | 38095_i_at |



|   |        |           |           |         |  |            |  |
|---|--------|-----------|-----------|---------|--|------------|--|
|   |        |           |           |         |  | /len=1501  |  |
| HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)  | M83664 | Hs.814    | NM_002121 | 6p21.3  | Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501 | 38096_f_at |  |
| MPO (myeloperoxidase)   | M19507 | Hs.1817   | NM_000250 | 17q23.1 | Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215                                     | 33284_at   |  |
| HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1) | X00457 | Hs.914    |           | 6p21.3  | Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048               | 38833_at   |  |
| AHR (aryl hydrocarbon receptor)                                   | L19872 | Hs.170087 | NM_001621 | 7p15    | Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,2921) /gb=L19872 /gi=416141 /ug=Hs.170087  | 40516_at   |  |

|  |          |           |           |          |  |  |            |
|--|----------|-----------|-----------|----------|--|--|------------|
|  |          |           |           |          |  | /len=5228  |            |
| DKFZP564K0822( hypothetical protein DKFZp564K0822 )      | WZ5986   | Hs.4750   | NM_030796 | 7        |  | Cluster Incl. WZ5986:17e7 Homo sapiens cDNA /gb=WZ5986 /gj=1306253 /ug=Hs.4750 /len=769  | 34830_at   |
| HOXA7 (homeo box A7)                                     | AC004080 | Hs.70954  | NM_006896 | 7p15-p14 |  | Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170019 from 7p15-p21 /cds=(0,1247) /gb=AC004080 /gj=2822164 /ug=Hs.110637 /len=1248                 | 41448_at   |
|  |          |           |           |          |  | Cluster Incl. AL096717:Homo sapiens mRNA; cDNA DKFZp564P0662 (from clone DKFZp564P0662) /cds=UNKNOWN /gb=AL096717 /gj=5419852 /ug=Hs.24178 /len=2228 | 41328_s_at |
| S100A9 (S100 calcium-binding protein A9 (calgranulin B)) | W72424   | Hs.112405 | NM_002965 | 1q21     |  | Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gj=1382379 /ug=Hs.112405 /len=604              | 41471_at   |

|   |          |           |           |              |   |          |
|---|----------|-----------|-----------|--------------|---|----------|
| CHD3 (chromodomain helicase DNA binding protein 3)            | U91543   | Hs.25601  | NM_001272 | 17p13.1      | Cluster Incl. U91543:Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds /cds=(150,6152) /gb=U91543 /gi=3298561 /ug=Hs.237761 /len=6771 | 34707_at |
| PPIB (peptidylprolyl isomerase B (cyclophilin B))             | M63573   | Hs.699    | NM_000942 | 15q21-q22    | Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671) /gb=M63573 /gi=337998 /ug=Hs.699 /len=893 | 35823_at |
| HLA-DMB (major histocompatibility complex, class II, DM beta) | U15085   | Hs.1162   | NM_002118 | 6p21.3       | Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362                               | 41609_at |
| TNFAIP3 (tumor necrosis factor, alpha-induced protein 3)      | M59465   | Hs.211600 | NM_006290 | 6q23.1-q25.3 | M59465 /FEATURE= /DEFINITION=HUMA20 Human tumor necrosis factor alpha inducible protein A20 mRNA, complete cds                                  | 595_at   |
| LGALS9 (lectin, galactoside-binding, soluble, 9 (galectin 9)) | AB006782 | Hs.81337  | NM_002308 | 17           | AB006782 /FEATURE= /DEFINITION=AB006782 Homo sapiens  | 766_at   |

| (galectin 9))   |          |           |           |         |  | mRNA for galectin-9 isoform, complete cds  |          |
|---|----------|-----------|-----------|---------|--|--|----------|
| RAD23A (RAD23 (S. cerevisiae) homolog A)  | D21235   | Hs.180455 | NM_005053 | 19p13.2 |  | Cluster Incl. D21235:Human mRNA for HHR23A protein, complete cds /cds=(36,1127) /gb=D21235 /gi=488145 /ug=Hs.180455 /len=1719  | 41197_at |
| SLC7A7 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 7) | AJ130718 | Hs.194693 | NM_003982 | 14q11.2 |  | Cluster Incl. AJ130718:Human sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1 /cds=(293,1828) /gb=AJ130718 /gi=3970724 /ug=Hs.194693 /len=2214 | 33731_at |
| BMI1 (murine leukemia viral (bmi-1) oncogene homolog)                                   | L13689   | Hs.431    | NM_005180 | 10p13   |  | Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cds=(479,1459) /gb=L13689 /gi=291872 /ug=Hs.431 /len=3203                                       | 41562_at |
| DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase)                   | D29643   | Hs.34789  | NM_005216 | 1p36.1  |  | Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936  | 38791_at |

|   |        |           |           |         |   |                        |  |  |  |            |
|---|--------|-----------|-----------|---------|---|------------------------|--|--|--|------------|
|   |        |           |           |         |   | /ug=Hs.89674 /len=1668 |  |  |  | 36105_at   |
| CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)) | M18728 | Hs.73848  | NM_002483 | 19q13.2 | Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533 |                        |  |  |  |            |
| TPM4 (tropomyosin 4)  | X05276 | Hs.250641 | NM_003290 | 19p13.1 | Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049           |                        |  |  |  | 33866_at   |
| CD34 (CD34 antigen)   | M81945 | Hs.85289  | NM_001773 | 1q32    | Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616                           |                        |  |  |  | 38747_at   |
| HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)  | M32578 | Hs.180255 | NM_002124 | 6p21.3  | Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216      |                        |  |  |  | 41723_s_at |

|   |          |           |           |               |  |            |
|---|----------|-----------|-----------|---------------|--|------------|
| SIAT4C (sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase))            | X74570   | Hs.75268  | NM_006278 | 11q23-q24     | Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741 | 36916_at   |
| RGS10 (regulator of G-protein signalling 10)  | AF045229 | Hs.82280  | NM_002925 | 10q25         | Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753 | 33121_g_at |
| EBI2 (Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)) | L08177   | Hs.784    | NM_004951 | 13            | L08177 /FEATURE= /DEFINITION=HUMGPCRB Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds   | 931_at     |
| NUCB1 (nucleobindin 1)  | M96824   | Hs.172609 | NM_006184 | 19q13.2-q13.4 | Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650                        | 40817_at   |

|   |        |          |           |          |   |          |
|---|--------|----------|-----------|----------|---|----------|
| PGRMC1 (progesterone receptor membrane component 1)                 | Y12711 | Hs.90061 | NM_006667 | xq22-q24 | Cluster Incl. Y12711:H.sapiens mRNA for putative progesterone binding protein /cds=(51,638) /gb=Y12711 /gi=2062021 /ug=Hs.90061 /len=1924       | 38802_at |
| CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8) | M33326 | Hs.41    | NM_001816 | 19q13.2  | Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287 | 33630_at |
| HLA-DMA (major histocompatibility complex, class II, DM alpha)      | X62744 | Hs.77522 | NM_006120 | 6p21.3   | Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079       | 37344_at |
| DKFZP586N1922( DKFZP586N1922 protein                                | N99340 | Hs.7357  |           | 19       | Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110                              | 36095_at |

|   |          |           |           |             |  |          |
|---|----------|-----------|-----------|-------------|--|----------|
| SLC9A3R1 (solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1) | AF015926 | Hs.184276 | NM_004252 | 17          | Cluster Incl. AF015926:Homo sapiens ezrin-radixin-moesin phosphoprotein-50 mRNA, complete cds /cds=(212,1288) /gb=AF015926 /gi=3220018 /ug=Hs.184276 /len=1984 | 32174_at |
| MEL (mel transforming oncogene (derived from cell line NK14)- RAB8 homolog)                   | AI819948 | Hs.5947   | NM_005370 | 19p13.1     | Cluster Incl. AI819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409932 /clone_end=3 /gb=AI819948 /gi=5439027 /ug=Hs.5947 /len=569                     | 35340_at |
| LYPLA1 (lysophospholipase I)  | AF081281 | Hs.12540  | NM_006330 | 6pter-p25.1 | Cluster Incl. AF081281:Homo sapiens lysophospholipase (LPL1) mRNA, complete cds /cds=(35,727) /gb=AF081281 /gi=3415122 /ug=Hs.12540 /len=2417                  | 39396_at |
| PSCDBP (pleckstrin homology, Sec7 and coiled/coil domains, binding protein)                   | AF068836 | Hs.270    | NM_004288 | 2q11.2      | Cluster Incl. AF068836:Homo sapiens cytohesin binding protein HE mRNA, complete cds /cds=(33,1112) /gb=AF068836 /gi=3192908 /ug=Hs.270                         | 39804_at |



|  |        |           |           |             |  |  |          |
|--|--------|-----------|-----------|-------------|--|--|----------|
|  |        |           |           |             |  | /len=1771  |          |
|  |        |           |           |             |  | Cluster Incl. M22806:Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene /cds=(66,1592) /gb=M22806 /gi=487831 /ug=Hs.75655 /len=2438 | 36666_at |
| CXX1 (CAAX box 1)  | Y13374 | Hs.250708 | NM_003928 | xq26        |  | Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protein /cds=(343,972) /gb=Y13374 /gi=2370152 /ug=Hs.239533 /len=1186                       | 33856_at |
| SERPING1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)) | X54486 | Hs.151242 | NM_000062 | 11q12-q13.1 |  | Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827   | 39775_at |
| KIAA0088( KIAA0088 protein )   | D42041 | Hs.76847  | NM_014610 | 11          |  | Cluster Incl. D42041:Human mRNA for KIAA0088 gene, partial cds /cds=(0,2832) /gb=D42041 /gi=577294 /ug=Hs.76847  | 37040_at |

|  |        |           |           |         |  |   |            |  |  |
|--|--------|-----------|-----------|---------|--|---|------------|--|--|
|  |        |           |           |         |  | /len=3820   |            |  |  |
| MTCP1 (mature T-cell proliferation 1)  | Z24459 | Hs.3548   | NM_014221 | xq28    |  | Cluster Incl. Z24459:H.sepiens MTCP1 gene, exons 2A to 7 (and joined mRNA) /cds=(1419,1625) /gb=Z24459 /gi=2252491 /ug=Hs.3548 /len=1847      | 35688_g_at |  |  |
| NFKBIA (nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha) | M69043 | Hs.81328  | NM_020529 | 14q13   |  | M69043 /FEATURE= /DEFINITION=HUMMAD3A Homo sapiens MAD-3 mRNA encoding IKB-like activity, complete cds  | 1461_at    |  |  |
| MST1 (macrophage stimulating 1 (hepatocyte growth factor-like))                              | U37055 | Hs.278657 | NM_020998 | 3p21    |  | U37055 /FEATURE=mRNA Human /DEFINITION=HSU37055 Human hepatocyte growth factor-like protein gene, complete cds                                | 1047_s_at  |  |  |
| ABR (active BCR-related gene)  | U01147 | Hs.118021 | NM_001092 | 17p13.3 |  | Cluster Incl. U01147:Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds /cds=(110,2689) /gb=U01147 /gi=393094 /ug=Hs.118021 | 39058_at   |  |  |

|   |        |          |           |               |  |                            |           |
|---|--------|----------|-----------|---------------|--|----------------------------|-----------|
|   |        |          |           |               |  | /len=5242                  |           |
| TRA1 (tumor rejection antigen (gp96) 1)               | X15187 | Hs.82689 | NM_003299 | 12q24.2-q24.3 | X15187<br>/DEFINITION=HSTRA1<br>mRNA for human homologue of murine<br>tumor rejection antigen gp96 | /FEATURE=cds<br>Human tra1 | 442_at    |
| CEBPD (CCAAT/enhancer binding protein (C/EBP), delta) | M83667 | Hs.76722 | NM_005195 | 8p11.2-p11.1  | M83667<br>/DEFINITION=HUMNFIL6BA<br>IL6-beta protein mRNA, complete cds                            | /FEATURE=mRNA<br>Human NF- | 1052_s_at |

Table 14:

| UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol | GenBank Accession No. | UniGene Cluster | RefSeq    | Chromosomal Location | Description Unigene Build #95   | Gene Name  |
|---|-----------------------|-----------------|-----------|----------------------|---|------------|
| CAMP (cathelicidin antimicrobial peptide)             | Z38026                | Hs.51120        | NM_004345 | 3p21.3               | Cluster Incl. Z38026; H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615                             | 36710_at   |
| MYH11 (myosin, heavy polypeptide 11, smooth muscle)   | AF001548              | Hs.78344        | NM_002474 | 16p13.13-p13.12      | AF001548 /FEATURE=mRNA /DEFINITION=HUA001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence  | 767_at     |
| MYH11 (myosin, heavy polypeptide 11, smooth muscle)   | AF013570              | Hs.78344        | NM_002474 | 16p13.13-p13.12      | Cluster Incl. AF013570; Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 | 37407_s_at |

|   |          |          |           |      |  |   |          |
|---|----------|----------|-----------|------|--|---|----------|
|   |          |          |           |      |  | /ug=Hs.78344 /len=2580  |          |
| SYNE-1B(synaptic nuclear envelope 1)      | AB018339 |          |           |      |  | Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900 | 38113_at |
|   | K03000   | Hs.76392 | NM_000689 | 9q21 |  | Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560                     | 37015_at |
| ARHGAP4 (Rho GTPase activating protein 4) | X78817   | Hs.3109  | NM_001666 | xq28 |  | Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236                               | 39649_at |
| LIG1 (ligase I, DNA, ATP-dependent)       | AL039458 | Hs.4193  |           | 3p14 |  | Cluster Incl. AL039458:DKFZp434N0910_s1 sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 /gb=AL039458 /gi=5408506 /ug=Hs.4193      | 34800_at |

|   |          |           |           |          |   |            |  |
|---|----------|-----------|-----------|----------|---|------------|--|
|   |          |           |           |          |   | /len=849   |  |
| CTSW (cathepsin W (lymphopain))                   | AF013611 | Hs.87450  | NM_001335 | 11q13.1  | Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131   | 40718_at   |  |
| LON2 (lipocalin 2 (oncogene 24p3))                | A1762213 | Hs.204238 | NM_005564 | 9q34     | Cluster Incl. A1762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=A1762213 /gi=5177880 /ug=Hs.204238 /len=677  | 32821_at   |  |
| CCR2 (chemokine (C-C motif) receptor 2)           | U95626   |           |           | 3p21     | Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607 | 37149_s_at |  |
| PBX3 (pre-B-cell leukemia transcription factor 3) | X59841   | Hs.294101 | NM_006195 | 9q33-q34 | Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314  | 32696_at   |  |

|   |          |           |           |              |  |  |          |
|---|----------|-----------|-----------|--------------|--|--|----------|
|   |          |           |           |              |  | /ug=Hs.171680 /len=2581  |          |
| CBX7 (chromobox homolog 7)  | AL031846 | Hs.395    | NM_000647 | 22q13.1      |  | Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gj=4164368 /ug=Hs.7442 /len=3964                 | 36894_at |
| SGP28( specific granule protein (28 kDa); cysteine-rich secretory protein-3 ) | X94323   | Hs.54431  | NM_008061 |              |  | Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gj=1213612 /ug=Hs.54431 /len=2124                        | 36464_at |
| PLCE2 (phospholipase C, epsilon 2)  | AB029015 | Hs.54886  |           | 3p25.3-p25.1 |  | Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gj=5689520 /ug=Hs.54886 /len=4147 | 41796_at |
| KIAA0246( KIAA0246 protein )  | D87433   | Hs.301989 | NM_015136 |              |  | Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gj=1665760 /ug=Hs.84753 /len=6777               | 38487_at |

|   |          |           |           |          |   |            |
|---|----------|-----------|-----------|----------|---|------------|
| PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective | M54995   | Hs.2164   | NM_002704 | 4q12-q13 | Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673           | 39209_r_at |
| KIAA0906( KIAA0906 p  | AB020713 | Hs.56866  |           |          | Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56866 /len=4217                  | 41812_s_at |
| KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)                        | AF052728 | Hs.188021 | NM_000238 | 7q35-q36 | Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767 | 38225_at   |
| CDW52 (CDW52 antigen (CAMPATH-1 antigen))   | N90866   | Hs.276770 | NM_001803 | 1p36     | Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577                  | 34210_at   |



|   |           |           |           |           |   |            |
|---|-----------|-----------|-----------|-----------|---|------------|
| PLSCR1 (phospholipid scramblase 1)  | AB0006746 | Hs.198282 | NM_021105 | 3q23      | Cluster Incl. AB0006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB0006746 /gi=3510296 /ug=Hs.198282 /len=2077              | 32775_r_at |
| PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective | M54995    | Hs.2164   | NM_002704 | 4q12-q13  | Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673 | 39208_l_at |
| PLXNB2 (plexin B2)  | AB002313  | Hs.3989   |           | 22q13.33  | Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252                   | 34780_at   |
| TRB@ (T cell receptor beta locus)   | M12886    | Hs.303157 |           | Hs.303157 | M12886 /FEATURE= /DEFINITION=HUMTCBY Human T-cell receptor active beta-chain mRNA, complete cds   | 1105_s_at  |
| NS1-BP( NS1-binding protein )   | AB020657  | Hs.197298 | NM_006469 |           | Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds   | 33752_at   |

|  |          |           |           |         |  |  |  |  |  |   |            |
|--|----------|-----------|-----------|---------|--|--|--|--|--|---|------------|
|  |          |           |           |         |  | /cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682 |  |  |  | Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802 | 39756_g_at |
| XBP1 (X-box binding protein 1)                       | Z93930   | Hs.149923 | NM_005080 | 22q12.1 |  |  |  |  |  |   |            |
| SYNE-2( synaptic nuclear expressed gene 2 )          | AL080133 | Hs.57749  | NM_015180 |         |  |  |  |  |  | Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307   | 41815_at   |
| HLA-F (major histocompatibility complex, class I, F) | AL022723 | Hs.110309 | NM_018950 | 6p21.3  |  |  |  |  |  | Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723  | 37420_i_at |

|   |        |          |           |          |  |          |
|---|--------|----------|-----------|----------|--|----------|
|   |        |          |           |          | /gi=5002624 /ug=Hs.110309 /len=1303  |          |
| AOE372( thioredoxin peroxidase (antioxidant enzyme) )                               | U25182 | Hs.83383 | NM_006406 |          | Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921   | 38435_at |
| SELL (selectin L (lymphocyte adhesion molecule 1))                                  | M25280 | Hs.82848 | NM_000655 | 1q23-q25 | M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds   | 245_at   |
| PF4 (platelet factor 4)   | M25897 | Hs.81564 | NM_002619 | 4q12-q21 | M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) mRNA, complete cds  | 1115_at  |
| SERPINB6 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6) | S69272 | Hs.41072 | NM_004568 | 6p25     | Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072 | 34789_at |

|   |          |           |           |           |  |           |  |
|---|----------|-----------|-----------|-----------|--|-----------|--|
|   |          |           |           |           |  | /len=1465 |  |
| HOXB2 (homeo box B2)  | X16665   | Hs.2733   | NM_002145 | 17q21-q22 | Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520                          | 39610_at  |  |
| S100A8 (S100 calcium-binding protein A8 (calgranulin A))  | A1126134 | Hs.100000 | NM_002964 | 1q21      | Cluster Incl. A1126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=A1126134 /gi=3594648 /ug=Hs.100000 /len=446 | 41096_at  |  |
| CD59 (CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 | M84349   | Hs.119863 | NM_000611 | 11p13     | Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,404) /gb=M84349 /gi=180150 /ug=Hs.119863 /len=1840                     | 39351_at  |  |
| GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))                     | M63904   | Hs.73797  | NM_002068 | 19p13.3   | Cluster Incl. M63904:Human G-alpha.16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891                                       | 40365_at  |  |

|   |          |           |           |        |  |  |            |
|---|----------|-----------|-----------|--------|--|--|------------|
|   |          |           |           |        |  | /ug=Hs.73797 /len=2060   |            |
| PIG6( proline oxidase homolog )                                       | AF010310 | Hs.274550 |           |        |  | Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888               | 34110_g_at |
|   | AF052169 |           |           |        |  | Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169 /gi=3360480 /ug=Hs.109438 /len=1385                          | 38972_at   |
| EIF4EL3 (eukaryotic translation initiation factor 4E-like 3)          | AF038957 | Hs.19122  | NM_004846 | 2q37.1 |  | Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961 | 32229_at   |
| DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase) | D29643   | Hs.34789  | NM_005216 | 1p36.1 |  | Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936  | 38791_at   |

|   |        |           |           |               |  |                        |          |  |
|---|--------|-----------|-----------|---------------|--|------------------------|----------|--|
|   |        |           |           |               |  | /ug=Hs.89674 /len=1668 |          |  |
| MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)) | J05070 | Hs.151738 | NM_004994 | 20q11.2-q13.1 | Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334   |                        | 31859_at |  |
| CALR (calreticulin  | M84739 | Hs.16488  | NM_004343 | 19p13.3-p13.2 | Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937  |                        | 32543_at |  |
| DKFZP564K0822( hypothetical protein DKFZp564K0822 )   | W25986 | Hs.4750   | NM_030796 |               | Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769  |                        | 34830_at |  |
| XBP1 (X-box binding protein 1)  | Z93930 | Hs.149923 | NM_005080 | 22q12.1       | Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) |                        | 39755_at |  |

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|--|----------|-----------|-----------|-----------------|---|---|--|--|--|------------|
|  |          |           |           |                 |   | /gb=Z93930 /gi=4775603 /ug=Hs.149923<br>/len=1802 |  |  |  | 36601_at   |
| VCL (vinculin)   | M33308   | Hs.75350  | NM_003373 | 10q22.1-q23     | Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250)<br>/gb=M33308 /gi=340236 /ug=Hs.75350<br>/len=5102  |   |  |  |  | 36601_at   |
| POU4F1 (POU domain, class 4, transcription factor 1)                 | L20433   | Hs.211588 | NM_006237 | 13q21.1-q22     | Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496)<br>/gb=L20433 /gi=418015 /ug=Hs.211588<br>/len=3824 |   |  |  |  | 35939_s_at |
| MIC2 (antigen identified by monoclonal antibodies 12E7, F21 and O13) | M16279   | Hs.177543 | NM_002414 | xp22.32, yp11.3 | Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M16279<br>/gi=188542 /ug=Hs.177543 /len=1238  |   |  |  |  | 41138_at   |
| DEFA4 (defensin, alpha 4, corticostatin)                             | A1250799 | Hs.2582   | NM_001925 | 8p23            | Cluster Incl. A1250799:q136g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-  |   |  |  |  | 34546_at   |

|   |          |           |           |              |  |  |          |
|---|----------|-----------|-----------|--------------|--|--|----------|
|   |          |           |           |              |  | 1858620 /clone_end=3 /gb=A1250799 /gi=3847328 /ug=Hs.2582 /len=542   |          |
| NDUFC1 (NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (GkD, KFYI)) | AA760866 | Hs.84549  | NM_002494 | 4q28.2-q31.1 |  | Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549 /len=553                    | 38485_at |
| SPTA1 (spectrin, alpha, erythrocytic 1 (elliptocytosis 2))                    | M61877   | Hs.1985   | NM_003126 | 1q21         |  | Cluster Incl. M61877:Human erythroid alpha-spectrin (SPTA1) mRNA, complete cds /cds=(186,7475) /gb=M61877 /gi=338437 /ug=Hs.1985 /len=8001 | 38906_at |
| EPB72 (erythrocyte membrane protein band 7.2 (stomatin))                      | X85116   | Hs.160483 | NM_004099 | 9q34.1       |  | Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035                              | 40419_at |
| CD24 (CD24 antigen (small cell lung carcinoma cluster 4 antigen))             | L33930   | Hs.286124 | NM_013230 | 6q21         |  | L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region                                  | 266_s_at |



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|--|----------|-----------|-----------|---------------|--|----------|
| HOXA9 (homeo box A9)   | U41813   | Hs.127428 | NM_002142 | 7p15-p14      | Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411    | 37809_at |
| HLA-DRA (major histocompatibility complex, class II, DR alpha)   | J00194   | Hs.76807  | NM_019111 | 6p21.3        | Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199    | 37039_at |
| OLR1 (oxidised low density lipoprotein (lectin-like) receptor 1) | AF079167 | Hs.77729  | NM_002543 | 12p13.2-p12.3 | Cluster Incl. AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003 /ug=Hs.77729 /len=2468  | 37233_at |
|  | M1872    |           |           |               | Cluster Incl. M1872:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533 | 36105_at |
| DEK (DEK oncogene (DNA binding))                                 | X64229   | Hs.110713 | NM_003472 | 6p23          | Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502  | 38992_at |

|   |          |           |  |           |            |  |          |
|---|----------|-----------|--|-----------|------------|--|----------|
|   |          |           |  |           |            | /ug=Hs.110713 /len=2699  |          |
| AGRN (agrin)  | AF016903 | Hs.273330 |  |           | 1p36.3-p32 | Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032                             | 33454_at |
| PIR121( p53 inducible protein )   | L47738   | Hs.256503 |  |           |            | Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881                            | 37579_at |
| ITGB2 (integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage | M15395   | Hs.83968  |  | NM_000211 | 21q22.3    | Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381) /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776 | 37918_at |
| STAT12(cytokine inducible SH2-containing protein 2)   | AF037989 | Hs.110776 |  | NM_003877 |            | Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032                                     | 38994_at |

|   |          |           |           |  |              |   |          |
|---|----------|-----------|-----------|--|--------------|---|----------|
|   |          |           |           |  |              | /ug=Hs.110776 /len=1937   |          |
| TBC1D1 (TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1) | AB029031 | Hs.278586 |           |  | 4            | Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576          | 32508_at |
| DEFA1 (defensin, alpha 1, myeloid-related sequence)             | AL036554 | Hs.274463 | NM_004084 |  | 8p23.2-p23.1 | Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /done_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517   | 31793_at |
| MGC2747( hypothetical protein MGC2747 )                         | AL046940 | Hs.250723 | NM_024104 |  |              | Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /done_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695 | 41273_at |

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|---|----------|----------|-----------|----------|---|----------|
| LILRB2 (leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), | AF004231 | Hs.22405 | NM_005874 | 19q13.4  | Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds /cds=(208,2001) /gb=AF004231 /gi=2343110 /ug=Hs.22405 /len=2863 | 39221_at |
| CPA3 (carboxypeptidase A3 (mast cell))  | M73720   | Hs.646   | NM_001870 | 3q21-q25 | Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633   | 36749_at |
|   | M13560   |          |           |          | Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080  | 35016_at |
|   | M3332    |          |           |          | Cluster Incl. M3332:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287                                    | 33530_at |

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|--|----------|-----------|-----------|-------------|---|------------|
| DEFA3 (defensin, alpha 3, neutrophil-specific) | L12691   | Hs.294176 | NM_005217 | 8pter-p23.3 | Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds<br>/cds=(50,334) /gb=L12691 /gi=292364<br>/ug=Hs.178741 /len=452   | 31506_s_at |
| PLXNC1 (plexin C1)                             | AF030339 | Hs.286229 | NM_005761 | 12          | Cluster Incl. AF030339:Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds<br>/cds=(249,4955) /gb=AF030339<br>/gi=3176761 /ug=Hs.184697 /len=5121 | 32193_at   |
|  | U7066    |           |           |             | Cluster Incl. U70663:Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915)<br>/gb=U70663 /gi=1857160 /ug=Hs.236377<br>/len=1953              | 36214_at   |
|  | AF035315 |           |           |             | Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence<br>/cds=UNKNOWN /gb=AF035315<br>/gi=2661077 /ug=Hs.180737 /len=1331                                 | 33267_at   |

| CTSE (cathepsin E)  | J05036   | Hs.1355   | NM_001910 | 1q31          | J05036<br>/DEFINITION=HUMCTSE<br>cathepsin E mRNA, complete cds   | /FEATURE=mRNA<br>Human | 271_s_at |
|---|----------|-----------|-----------|---------------|---|------------------------|----------|
| NDUFB5 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDHI)) | AF047181 | Hs.19236  | NM_002492 | 3q25.1-q25.33 | Cluster Incl. AF047181: Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034 |                        | 32232_at |
| S100A9 (S100 calcium-binding protein A9 (calgranulin B))                    | W72424   | Hs.112405 | NM_002965 | 1q21          | Cluster Incl. W72424: zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604                            |                        | 41471_at |
| SNRPN (small nuclear ribonucleoprotein polypeptide N)                       | U41303   | Hs.48375  | NM_003097 | 15q12         | Cluster Incl. U41303: Human small nuclear ribonucleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326     |                        | 34842_at |

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|--|----------|-----------|-----------|-------------|---|------------|
| SLU7( step II splicing factor SLU7 )                 | AI660656 | Hs.76325  | NM_006425 |             | Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351436 /clone_end=3 /gb=AI660656 /gi=4764239 /ug=Hs.76325 /len=522 | 37006_at   |
| ADD2 (adducin 2 (beta))                              | U43959   | Hs.247423 | NM_001617 | 2p14-p13    | Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 /ug=Hs.4852 /len=1284 | 36052_at   |
| DF (D component of complement (adipsin))             | M84526   | Hs.155597 | NM_001928 | 19          | Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071       | 40282_s_at |
| PLCB2 (phospholipase C, beta 2)                      | M95678   | Hs.994    | NM_004573 | 15q15       | M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-2 mRNA, complete cds   | 210_at     |
| POU4F1 (POU domain, class 4, transcription factor 1) | X64624   | Hs.211588 | NM_006237 | 13q21.1-q22 | Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein   | 35940_at   |

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| factor 1)   |          |          |           |           |  | /cds=(277,1272) /gb=X64624 /gi=35914<br>/ug=Hs.211588 /len=3492  |          |  |
| PPIB (peptidylprolyl isomerase B (cyclophilin B))     | M63573   | Hs.699   | NM_000942 | 15q21-q22 |  | Cluster Incl. M63573:Human secreted<br>cyclophilin-like protein (SCYLP) mRNA,<br>complete cds /cds=(21,671) /gb=M63573<br>/gi=337998 /ug=Hs.699 /len=893 | 35823_at |  |
| KIAA0088( KIAA0088 protein )                          | D42041   | Hs.76847 | NM_014610 |           |  | Cluster Incl. D42041:Human mRNA for<br>KIAA0088 gene, partial cds /cds=(0,2832)<br>/gb=D42041 /gi=577294 /ug=Hs.76847<br>/len=3820                       | 37040_at |  |
| LAK-4P( expressed in activated T/LAK<br>lymphocytes ) | AB002405 | Hs.16165 | NM_007267 |           |  | Cluster Incl. AB002405:Homo sapiens<br>mRNA for LAK-4p, complete cds<br>/cds=(109,1149) /gb=AB002405<br>/gi=2760120 /ug=Hs.16165 /len=1376               | 32116_at |  |
| TFDP1 (transcription factor Dp-1)                     | L23959   | Hs.79353 | NM_007111 | 13q34     |  | Cluster Incl. L23959:Homo sapiens E2F-<br>related transcription factor (DP-1) mRNA,<br>complete cds /cds=(37,1269) /gb=L23959                            | 37757_at |  |



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|---|----------|-----------|-----------|-----------|--|--|----------|
|   |          |           |           |           |  | /gi=414316 /ug=Hs.79353 /len=1440  |          |
| CPO (coproporphyrinogen oxidase (coproporphyrin, harderoporphyria))                             | D16611   | Hs.89866  | NM_000097 | 3q12      |  | Cluster Incl. D16611:Human mRNA for coproporphyrinogen oxidase, complete cds /cds=(93,1157) /gb=D16611 /gi=469488 /ug=Hs.89866 /len=2333                                   | 37999_at |
| MMP8 (matrix metalloproteinase 8 (neutrophil collagenase))                                      | J05556   | Hs.73862  | NM_002424 | 11q22.3   |  | J05556 /FEATURE=mRNA /DEFINITION=HUMCLGNA Homo sapiens collagenase mRNA, complete cds  | 681_at   |
| DUSP6 (dual specificity phosphatase 6)  | AB013382 | Hs.180383 | NM_001946 | 12q22-q23 |  | Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390  | 41193_at |
| NPR3 (natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)) | M59305   | Hs.123655 | NM_000908 | 5p14-p13  |  | Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651 /ug=Hs.123655 /len=2081 | 34519_at |

|   |          |           |           |         |   |          |
|---|----------|-----------|-----------|---------|---|----------|
| MPO (myeloperoxidase)   | M19507   | Hs.1817   | NM_000250 | 17q23.1 | Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215  | 33284_at |
| MINPP1 (multiple inositol polyphosphate histidine phosphatase, 1) | AL050356 | Hs.95907  | NM_004897 | 10q23   | Cluster Incl. AL050356: Homo sapiens mRNA; cDNA DKFZp564L2016 (from clone DKFZp564L2016) /cds=UNKNOWN /gb=AL050356 /gi=4914568 /ug=Hs.95907 /len=2396                                   | 38325_at |
|   | S67247   |           |           |         | Cluster Incl. S67247: smooth muscle myosin heavy chain isoform SMemb [human, umbilical cord, fetal aorta, mRNA Partial, 971 nt] /cds=(0,681) /gb=S67247 /gi=452986 /ug=Hs.2094 /len=971 | 32838_at |
| TPM4 (tropomyosin 4)  | X05276   | Hs.250641 | NM_003290 | 19p13.1 | Cluster Incl. X05276: Human mRNA for fibroblast tropomyosin TM30 (pi) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049  | 33866_at |

|   |          |           |           |             |   |          |
|---|----------|-----------|-----------|-------------|---|----------|
| CBFA2T1 (core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related) | D43638   | Hs.31551  | NM_004349 | 8q22        | Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460                          | 35638_at |
| LEF1 (lymphoid enhancer-binding factor 1)   | AL049409 | Hs.44865  | NM_016269 | 4q23-q25    | Cluster Incl. AL049409:Human sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419 | 36021_at |
| AHR (aryl hydrocarbon receptor)   | L19872   | Hs.170087 | NM_001621 | 7p15        | Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,2921) /gb=L19872 /gi=416141 /ug=Hs.170087 /len=5228                               | 40516_at |
| SERPINC1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1,            | X54486   | Hs.151242 | NM_000062 | 11q12-q13.1 | Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827  | 39775_at |
| PIG8(etoposide induced 2.4 mRNA)  | AF010313 | Hs.286027 | NM_004879 |             | Cluster Incl. AF010313:Human sapiens PIG8 (PIG8) mRNA, complete cds   | 38097_at |

|   |        |          |           |         |  |   |            |
|---|--------|----------|-----------|---------|--|---|------------|
|   |        |          |           |         |  | /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165   |            |
| SEPT3 (septin 3)                                      | Z99716 | Hs.8073  | NM_019106 | 22q13.2 |  | Cluster Incl. Z99716:bk250D10.5 (alpha-N-acetylglucosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606           | 36607_at   |
| TPM1 (tropomyosin 1 (alpha))                          | M19267 | Hs.77899 | NM_000366 | 15q22.1 |  | Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633                  | 36791_g_at |
| AMPD3 (adenosine monophosphate deaminase (isoform E)) | U29926 | Hs.83918 | NM_000480 | 11p15   |  | Cluster Incl. U29926:Human AMP deaminase (AMPD3) gene, promoter 1a region /cds=(453,2777) /gb=U29926 /gi=1002661 /ug=Hs.83918 /len=4018 | 38463_s_at |

|  |          |           |           |            |   |          |
|--|----------|-----------|-----------|------------|---|----------|
| HELO1( homolog of yeast long chain polunsaturated fatty acid elongation enzyme 2 | AL034374 | Hs.250175 | NM_021814 |            | Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL | 33821_at |
| PRKWNK1 (protein kinase, lysine deficient 1)                                     | U00946   | Hs.184592 | NM_018979 | 12p13.3    | Cluster Incl. U00946:Human clone AGA2BRB5 (CAC)n(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00946 /gi=405048 /ug=Hs.184592 /len=1971  | 32185_at |
| EPB41L2 (erythrocyte membrane protein band 4.1-like 2)                           | AF027299 | Hs.7857   | NM_001431 | 6q23       | Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /cds=(44,3061) /gb=AF027299 /gi=2739095 /ug=Hs.7857 /len=4316  | 32585_at |
| CD48 (CD48 antigen (B-cell membrane protein))                                    | M37766   | Hs.901    | NM_001778 | 1q21.3-q22 | Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds  | 38006_at |

|   |  |          |           |           |               |  |  |  |          |
|---|--|----------|-----------|-----------|---------------|--|--|--|----------|
|   |  |          |           |           |               | /cds=(20,751) /gb=M37766 /gi=187518<br>/ug=Hs.901 /len=1058  |  |  |          |
| PRDX2 (peroxiredoxin 2)                 |  | L19185   | Hs.146354 | NM_005809 | 13q12         | Cluster Incl. L19185:Human natural killer<br>cell enhancing factor- (NKEFB) mRNA,<br>complete cds /cds=(124,720) /gb=L19185<br>/gi=440307 /ug=Hs.146354 /len=980 |  |  | 39729_at |
| TIP30( Tat-interacting protein (30kD)   |  | AF039103 | Hs.90753  | NM_006410 |               | Cluster Incl. AF039103:Homo sapiens Tat-<br>interacting protein TIP30 mRNA, complete<br>cds /cds=(12,740) /gb=AF039103<br>/gi=3043926 /ug=Hs.90753 /len=1297     |  |  | 38824_at |
| ARG1 (arginase, liver)                  |  | M14502   | Hs.289057 | NM_000045 | 6q23          | M14502 /FEATURE=mRNA<br>/DEFINITION=HUMARGL Human liver<br>arginase mRNA, complete cds   |  |  | 1962_at  |
| TRA1 (tumor rejection antigen (gp96) 1) |  | X15187   | Hs.82689  | NM_003299 | 12q24.2-q24.3 | X15187 /FEATURE=cds<br>/DEFINITION=HSTRA1 Human tra1<br>mRNA for human homologue of murine<br>tumor rejection antigen gp96                                       |  |  | 442_at   |

|   |          |           |           |          |   |          |
|---|----------|-----------|-----------|----------|---|----------|
| HOXA7 (homeo box A7)  | AC004080 | Hs.70954  | NM_006896 | 7p15-p14 | Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170019 from 7p15-p21 /cds=(0,1247) /gb=AC004080 /gi=2822164 /ug=Hs.110637 /len=1248            | 41448_at |
| CD34 (CD34 antigen)   | M81945   | Hs.85289  | NM_001773 | 1q32     | Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616                                 | 38747_at |
| SNL (singled (Drosophila)-like (sea urchin fasciculation homolog like)) | U03057   | Hs.118400 | NM_003088 | 7p22     | Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767        | 39070_at |
| BZRP (benzodiazepine receptor (peripheral))                             | M36035   | Hs.202    | NM_000714 | 22q13.31 | Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035 /gi=194333 /ug=Hs.202 /len=811 | 32806_at |

|  |        |           |           |           |  |            |
|--|--------|-----------|-----------|-----------|--|------------|
| SIAT4C (sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)) | X74570 | Hs.75268  | NM_006278 | 11q23-q24 | Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741             | 36916_at   |
| TCF7 (transcription factor 7 (T-cell specific, HMG-box))                       | X59871 | Hs.169294 | NM_003202 | 5q31.1    | Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910                       | 32649_at   |
| HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)               | M83664 | Hs.814    | NM_002121 | 6p21.3    | Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501 | 38095_l_at |
| BMI1 (murine leukemia viral (bmi-1) oncogene homolog)                          | L13689 | Hs.431    | NM_005180 | 10p13     | Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cds=(479,1459) /gb=L13689 /gi=291872 /ug=Hs.431 /len=3203                             | 41562_at   |



|  |          |           |           |               |  |             |
|--|----------|-----------|-----------|---------------|--|-------------|
| RBM9 (RNA binding motif protein 9)                       | AL009266 | Hs.5011   | NM_014309 | 22q13.1       | Cluster Incl. AL009266:H. sapiens cDNA similar to C. elegans RNA binding protein U14946, Q10572, complete cds /cds=(170,1273) /gb=AL009266 /gi=2664428 /ug=Hs.155156 /len=1876 | 40260_g_at  |
| NUCB1 (nucleobindin 1)                                   | M96824   | Hs.172609 | NM_006184 | 19q13.2-q13.4 | Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650  | 40817_at    |
| IGF2R (insulin-like growth factor 2 receptor)            | Y00285   | Hs.76473  | NM_000876 | 6q26          | Y00285 /FEATURE=cds /DEFINITION=HSGFIIR Human mRNA for insulin-like growth factor II receptor /NOTE=replacement of probe set 972_s_at  | 160027_s_at |
| FCN1 (ficolin (collagen/fibrinogen domain-containing) 1) | S80990   | Hs.252136 | NM_002003 | 9q34          | Cluster Incl. S80990:ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1512) /gb=S80990 /gi=1911529 /ug=Hs.169237 /len=1723   | 36447_at    |

|   |          |         |           |               |  |          |
|---|----------|---------|-----------|---------------|--|----------|
| HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1) | X00457   | Hs.914  |           | 6p21.3        | Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048                 | 38833_at |
|   | M22806   |         |           |               | Cluster Incl. M22806:Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene /cds=(66,1592) /gb=M22806 /gi=487831 /ug=Hs.75655 /len=2438 | 36866_at |
|   |          |         |           |               | Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete cds /cds=(631,1866) /gb=AB011085 /gi=3043549 /ug=Hs.85053 /len=7758                  | 38735_at |
| MGEA5 (meningioma expressed antigen 5 (hyaluronidase))            | AB014579 | Hs.5734 | NM_012215 | 10q24.1-q24.3 | Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303                      | 35317_at |

Table 15:

| UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol          | GenBank Accession No. | UniGene Cluster | RefSeq    | Chromosomal Location | Description Unigene Build #95  | Gene Name |
|--|-----------------------|-----------------|-----------|----------------------|--|-----------|
| TNFRSF7 (tumor necrosis factor receptor superfamily, member 7) | M63928                | Hs.180841       | NM_001242 | 12p13                | Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204 | 38578_at  |
| DKFZP564K0822( hypothetical protein DKFZp564K0822 )            | W25986                | Hs.4750         | NM_030796 | 7                    | Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769  | 34830_at  |
| PFTK1 (PFTAIRE protein kinase 1)                               | AB020641              | Hs.57856        | NM_012395 | 7q21-q22             | Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957        | 36502_at  |

|   |          |           |  |              |   |            |
|---|----------|-----------|--|--------------|---|------------|
| CBX7 (chromobox homolog 7)              | AL031846 |           |  | 22q13.1      | Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964  | 36894_at   |
| IGHM (immunoglobulin heavy constant mu) | X58529   | Hs.302063 |  | 14q32.33     | Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325 | 41166_at   |
| PLCE2 (phospholipase C, epsilon 2)      | AB029015 | Hs.54886  |  | 3p25.3-p25.1 | Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147                            | 41796_at   |
| IGHM (immunoglobulin heavy constant mu) | X67301   | Hs.302063 |  | 14q32.33     | Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453                           | 41165_g_at |

|   |        |           |           |          |  |          |
|---|--------|-----------|-----------|----------|--|----------|
| IGHM (immunoglobulin heavy constant mu)                       | X67301 | Hs.302063 |           | 14q32.33 | Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453            | 41164_at |
|   |        |           |           |          | Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6-sialyltransferase /cds=(310,1530) /gb=X62822 /gi=29433 /ug=Hs.2554 /len=2699 | 41352_at |
| HLA-DOB (major histocompatibility complex, class II, DO beta) | X03066 | Hs.1802   | NM_002120 | 6p21.3   | Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chain /cds=(56,877) /gb=X03066 /gi=32271 /ug=Hs.1802 /len=1322                    | 38570_at |
|   | W30677 |           |           |          | Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614                | 34871_at |

|  |          |           |           |         |  |          |
|--|----------|-----------|-----------|---------|--|----------|
| IL24 (interleukin 24)  | AA214546 | Hs.315463 | NM_006850 | 1q32    | Cluster Incl. AA214546:zf92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516   | 41847_at |
| CELSR1 (cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog) | AL031588 | Hs.252387 | NM_014246 | 22q13.3 | Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438 | 41660_at |
| LOC54103( hypothetical protein )   | AL079277 | Hs.12969  |           | 7       | Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605 /cds=(0,806) /gb=AL079277 /gi=5102581 /ug=Hs.12969 /len=1414   | 41710_at |
| NIFU( nitrogen fixation cluster-like )   | U47101   | Hs.9908   |           | 12      | Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101   | 39165_at |

|   |          |           |           |         |  |  |          |  |  |
|---|----------|-----------|-----------|---------|--|--|----------|--|--|
|   |          |           |           |         |  | /ug=Hs.9908 /len=819   |          |  |  |
| CD79A (CD79A antigen (immunoglobulin-associated alpha)) | U05259   | Hs.79630  | NM_001783 | 19q13.2 |  | Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107  | 38017_at |  |  |
| SETBP1 (SET binding protein 1)                          | AB022660 | Hs.151717 | NM_015559 | 18q21.1 |  | Cluster Incl. AB022660: Homo sapiens mRNA for SET-binding protein (SEB), complete cds /cds=(5,4633) /gb=AB022660 /gi=5478317 /ug=Hs.151717 /len=5744       | 34990_at |  |  |
| NCOA3 (nuclear receptor coactivator 3)                  | AF012108 | Hs.225977 | NM_006534 | 20q12   |  | Cluster Incl. AF012108: Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds /cds=(200,4462) /gb=AF012108 /gi=2331249 /ug=Hs.225977 /len=6818 | 33381_at |  |  |
| POU2AF1 (POU domain, class 2, associating factor 1)     | Z49194   | Hs.2407   | NM_006235 | 11q23.1 |  | Cluster Incl. Z49194: H. sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407   | 36239_at |  |  |

|  |          |           |           |        |   |           |  |
|--|----------|-----------|-----------|--------|---|-----------|--|
|  |          |           |           |        |   | /len=3301 |  |
| SYNE-2( synaptic nuclei expressed gene 2 ) | AL080133 | Hs.57749  | NM_015180 | 22     | Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307   | 41815_at  |  |
| SP140( nuclear body protein Sp140 )        | U36500   | Hs.309943 | NM_007237 | 2      | Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.65283 /len=3252 | 40700_at  |  |
| CAMP (cathelicidin antimicrobial peptide)  | Z38026   | Hs.51120  | NM_004345 | 3p21.3 | Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615                            | 36710_at  |  |
| TOSO( regulator of Fas-induced apoptosis ) | AF057557 | Hs.58831  | NM_005449 | 1      | Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds /cds=(19,1191)   | 32967_at  |  |



|  |  |  |  |  |  |   |  |            |
|--|--|--|--|--|--|---|--|------------|
|  |  |  |  |  |  | /gb=AF057557<br>/ug=Hs.238857 /len=1339 | /gi=3169292  |            |
| TC21( oncogene TC21 )                      |  |  |  |  |  |   | Cluster Incl. AI365215;qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2029426 /clone_end=3 /gb=AI365215 /gi=4124904 /ug=Hs.206097 /len=918 | 32827_at   |
|  |  |  |  |  |  |   | Cluster Incl. AI434146;ti36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2132604 /clone_end=3 /gb=AI434146 /gi=4294137 /ug=Hs.164284 /len=299 | 36403_s_at |
| DGKA (diacylglycerol kinase, alpha (80kD)) |  |  |  |  |  |   | Cluster Incl. X62535;H.sapiens mRNA for diacylglycerol kinase /cds=(103,2310) /gb=X62535 /gi=30822 /ug=Hs.172690 /len=2564                   | 32716_at   |
| SAC2(cDNA sequence, clone 3-26)            |  |  |  |  |  |   | Cluster Incl. AB023183;Homo sapiens mRNA for KIAA0966 protein, complete cds /cds=(166,3564) /gb=AB023183                                     | 36089_at   |

|   |          |           |  |           |            |  |          |
|---|----------|-----------|--|-----------|------------|--|----------|
|   |          |           |  |           |            | /gi=4589575 /ug=Hs.52463 /len=4924   |          |
| SYNE-1B(synaptic nuclear envelope 1)            | AB018339 | Hs.8182   |  |           | 6          | Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900      | 38113_at |
| MSF (MLL sep/in-like fusion)                    | AB023208 | Hs.181002 |  | NM_006640 | 17q25      | Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938 | 41220_at |
| BCL2 (B-cell CLL/lymphoma 2)                    | M14745   | Hs.79241  |  | NM_000633 | 18q21.3    | M14745 /FEATURE= /DEFINITION=HUMBCL2C Human bcl-2 mRNA   | 1909_at  |
| E2F5 (E2F transcription factor 5, p130-binding) | U31556   | Hs.2331   |  | NM_001951 | 8p22-q21.3 | Cluster Incl. U31556:Human transcription factor E2F-5 mRNA, complete cds /cds=(38,1075) /gb=U31556 /gi=939728 /ug=Hs.2331 /len=1728          | 41275_at |

|  |          |           |           |               |   |           |
|--|----------|-----------|-----------|---------------|---|-----------|
| E2F5 (E2F transcription factor 5, p130-binding)  | U31556   | Hs.2331   | NM_001951 | 8p22-q21.3    | U31556<br>/DEFINITION=HSU31556<br>transcription factor E2F-5 mRNA,<br>complete cds  | 1044_s_at |
| IL4R (interleukin 4 receptor)  | X52425   | Hs.75545  | NM_000418 | 16p11.2-12.1  | X52425<br>/DEFINITION=HSIL4R Human IL-4-R<br>mRNA for the interleukin 4 receptor  | 404_at    |
| TLK1 (tousled-like kinase 1)   | D50927   | Hs.18895  | NM_012290 | 8p22-p12      | Cluster Incl. D50927:Human mRNA for<br>KIAA0137 gene, complete cds<br>/cds=(1088,2737) /gb=D50927<br>/gi=1469196 /ug=Hs.18895 /len=4454 | 32219_at  |
| MMP9 (matrix metalloproteinase 9 (gelatinase<br>B, 92kD gelatinase, 92kD type IV collagenase)) | J05070   | Hs.151738 | NM_004994 | 20q11.2-q13.1 | Cluster Incl. J05070:Human type IV<br>collagenase mRNA, complete cds<br>/cds=(19,2142) /gb=J05070 /gi=177204<br>/ug=Hs.151738 /len=2334 | 31859_at  |
| SH3BP5 (SH3-domain binding protein 5 (BTK-<br>associated))                                     | AB005047 | Hs.109150 | NM_004844 | 1q43          | Cluster Incl. AB005047:Homo sapiens<br>mRNA for SH3 binding protein, complete<br>cds /cds=(63,1340) /gb=AB005047                        | 38968_at  |

|   |          |           |           |    |  |   |            |
|---|----------|-----------|-----------|----|--|---|------------|
|   |          |           |           |    |  | /gi=3116213 /ug=Hs.108150 /len=2570   |            |
| GGA2( Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2   | AB029003 | Hs.155546 | NM_015044 | 16 |  | Cluster Incl. AB029003:Homo sapiens mRNA for KIAA1080 protein, partial cds /cds=(0,1554) /gb=AB029003 /gi=5689496 /ug=Hs.155546 /len=4791 | 40278_at   |
| SGP28( specific granule protein (28 kDa); cysteine-rich secretory protein-3 ) | X94323   | Hs.54431  | NM_006061 | 6  |  | Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124                         | 36464_at   |
| KIAA0430( KIAA0430 gene product )   | AB007890 |           |           | 16 |  | Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438 /ug=Hs.166163 /len=6011            | 31936_s_at |
|   | U92981   |           |           |    |  | Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429        | 38577_at   |

|   |          |           |           |               |   |           |
|---|----------|-----------|-----------|---------------|---|-----------|
| E2F5 (E2F transcription factor 5, p130-binding)             | U15642   | Hs.2331   | NM_001951 | 8p22-q21.3    | U15642<br>/DEFINITION=HSU15642<br>transcription factor E2F-5 mRNA,<br>complete cds  | 1639_s_at |
| ABCA6 (ATP-binding cassette, sub-family A (ABC1), member 6) | A1651024 | Hs.15780  |           | 17q21         | Cluster Inc. A1651024;wa86h06.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2304059 /clone_end=3' /gb=A1651024 /gij=4735003 /ug=Hs.15780 /len=657 | 35390_at  |
| EZH1 (enhancer of zeste (Drosophila) homolog 1)             | AB002386 | Hs.194669 | NM_001991 | 17q21.1-q21.3 | Cluster Inc. AB002386:Human mRNA for KIA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gij=2224716 /ug=Hs.194669 /len=4606             | 32259_at  |
| CD19 (CD19 antigen)   | M28170   | Hs.96023  | NM_001770 | 16p11.2       | M28170<br>/DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds   | 1086_g_at |
| PRDM2 (PR domain containing 2, with ZNF domain)             | D45132   | Hs.26719  | NM_012231 | 1p36          | D45132<br>/DEFINITION=HUMHOXY1 Homo sapiens   | 316_g_at  |

| domain)  |          |          |           |          |  | mRNA for zinc-finger DNA-binding protein, complete cds   |          |
|--|----------|----------|-----------|----------|--|--|----------|
| PSCD1 (pleckstrin homology, Sec7 and coiled/coiled domains 1(cytchesin 1)) | M85169   | Hs.1050  | NM_004762 | 17q25    |  | Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, - complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301         | 38666_at |
| KIAA0136(DNA segment, Chr 16, Johns Hopkins University 32, expressed)      | D50926   | Hs.70359 |           | 21q22.13 |  | Cluster Incl. D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,2854) /gb=D50926 /gi=1469194 /ug=Hs.70359 /len=4197                 | 36845_at |
| TGFB3 (transforming growth factor, beta receptor III (betaglycan, 300kD))  | L07594   | Hs.79059 | NM_003243 | 1p33-p32 |  | L07594 /FEATURE= Human /DEFINITION=HUMTGF3C transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete cds                | 1897_at  |
| DKFZP586F2423( hypothetical protein  | AL080209 | Hs.13659 |           | 7        |  | Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN /gb=AL080209 /gi=5262698 /ug=Hs.13659 | 39692_at |

|                                    |          |           |           |      |   |           |  |  |
|------------------------------------|----------|-----------|-----------|------|---|-----------|--|--|
|                                    |          |           |           |      |   | /len=4241 |  |  |
| AIM2 (absent in melanoma 2)        | AF024714 | Hs.105115 | NM_004833 | 1q22 | Cluster Incl. AF024714:Homo sapiens interferon-inducible protein (AIM2) mRNA, complete cds /cds=(245,1276) /gb=AF024714 /gi=2558941 /ug=Hs.105115 /len=1485 | 34439_at  |  |  |
| LCN2 (lipocalin 2 (oncogene 24p3)) | AI762213 | Hs.204238 | NM_005564 | 9q34 | Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677                | 32821_at  |  |  |
| KIAA0922( KIAA0922 protein )       | AB023139 | Hs.37892  | NM_015196 | 4    | Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505                    | 39929_at  |  |  |
| KIAA0769( KIAA0769 gene product )  | AB018312 | Hs.18056  | NM_014824 | 11   | Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete cds /cds=(239,2293) /gb=AB018312  | 32224_at  |  |  |

|   |          |           |           |                 |  |   |            |
|---|----------|-----------|-----------|-----------------|--|---|------------|
|   |          |           |           |                 |  | /gi=3882258 /ug=Hs.19056 /len=4326  |            |
| KIAA0746( KIAA0746 protein )                                      | AB018289 | Hs.49500  |           | 4               |  | Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212 /ug=Hs.49500 /len=4086                    | 41585_at   |
| FCER2 (Fc fragment of IgE, low affinity II, receptor for (CD23A)) | M15059   | Hs.1416   | NM_002002 | 19p13.3         |  | Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope) /cds=(213,1178) /gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530 | 34960_q_at |
| AKAP11 (A kinase (PRKA) anchor protein 11)                        | AB014529 | Hs.232076 | NM_016248 | 13q12.2-13q14.3 |  | Cluster Incl. AB014529:Homo sapiens mRNA for KIAA0629 protein, partial cds /cds=(0,1840) /gb=AB014529 /gi=3327071 /ug=Hs.232076 /len=5883                   | 34857_at   |
| KIAA0543( KIAA0543 protein )                                      | AB011115 | Hs.98507  |           | 7               |  | Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial cds /cds=(0,3336) /gb=AB011115 /gi=3043609   | 41077_at   |



|   |          |           |  |           |               |   |  |           |
|---|----------|-----------|--|-----------|---------------|---|--|-----------|
|   |          |           |  |           |               | /ug=Hs.98507 /len=6443  |  |           |
| PIR121( p53 inducible protein )                           | L47738   | Hs.258503 |  |           | 5             | Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881   |  | 37579_at  |
| MAP3K5 (mitogen-activated protein kinase kinase kinase 5) | U67156   | Hs.151988 |  | NM_005923 | 6q22.33       | U67156 /FEATURE= Human /DEFINITION=HSU67156 Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds                 |  | 1327_s_at |
| FLJ22531( hypothetical protein FLJ22531 )                 | W80358   | Hs.55613  |  | NM_024650 | 11            | Cluster Incl. W80358:zh49a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-415380 /clone_end=3 /gb=W80358 /gi=1391395 /ug=Hs.55613 /len=547  |  | 41804_at  |
| MGEA5 (meningioma expressed antigen 5 (hyaluronidase))    | AB014579 | Hs.5734   |  | NM_012215 | 10q24.1-q24.3 | Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303 |  | 35317_at  |

|   |          |           |           |             |  |           |
|---|----------|-----------|-----------|-------------|--|-----------|
| MDS019( phorbolin-like protein MDS019 ) | AL078641 | Hs.250619 | NM_021822 | 22          | Cluster Incl. AL078641:Human DNA sequence from clone 494G10 on chromosome 22 Contains part of a gene similar to phorbolin 2, ESTs and a GSS /cds=(0,419) /gb=AL078641 /gi=5162948 /ug=Hs.112449 /len=751 | 41472_at  |
| KIAA0240( KIAA0240 protein )            | D87077   | Hs.196275 |           | 6           | Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0,2853) /gb=D87077 /gi=1510154 /ug=Hs.196275 /len=6060  | 38892_at  |
| PRKCB1 (protein kinase C, beta 1)       | X07109   | Hs.77202  | NM_002738 | 16p11.2     | X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II /NOTE=replacement of probe set 1216_at   | 160029_at |
| CCR7 (chemokine (C-C motif) receptor 7) | L31584   | Hs.1652   | NM_001838 | 17q12-q21.2 | L31584 /FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled receptor (EBI 1) gene exon 3, complete cds  | 1097_s_at |

|   |          |           |           |       |  |                      |
|---|----------|-----------|-----------|-------|--|----------------------|
| CDC25B (cell division cycle 25B)        | S78187   | Hs.153752 | NM_004358 | 20p13 | S78187<br>/DEFINITION=S78187<br>CDC25Hu2=cdc25+ homolog [human,<br>mRNA, 3118 nt]  | /FEATURE=<br>1347_at |
| CCR2 (chemokine (C-C motif) receptor 2) | U95626   | Hs.395    | NM_000647 | 3p21  | Cluster Incl. U95626:Homo sapiens ccr2b<br>(ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6<br>(ccr6) genes, complete cds, and lactoferrin<br>(lactoferrin) gene, partial cds<br>/cds=(2,1429) /gb=U95626 /gi=2104517<br>/ug=Hs.105938 /len=1607 | 37149_s_at           |
|   | AL049701 |           |           |       | Cluster Incl. AL049701:Human gene from<br>PAC 433G19, chromosome 1 /cds=(0,370)<br>/gb=AL049701 /gi=4678835<br>/ug=Hs.107325 /len=648  | 34446_at             |
| P2Y10( putative purinergic receptor )   | AF000545 | Hs.296433 | NM_014499 | X     | AF000545<br>/DEFINITION=HSAF000545 Homo<br>sapiens putative purinergic receptor<br>P2Y10 gene, complete cds  | 358_at               |

|   |          |           |           |      |   |          |
|---|----------|-----------|-----------|------|---|----------|
| MGC12335( hypothetical protein MGC12335 )   | AL022724 | Hs.97411  | NM_032744 | 6    | Cluster Incl. AL022724:Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs /cds=(94,861) /gb=AL022724 /gi=4468306 /lug=Hs.97411 /len=1037 | 34043_at |
| P2Y10( putative purinergic receptor )       | Z82200   | Hs.296433 | NM_014499 | X    | Cluster Incl. Z82200:Human DNA sequence from clone 333E23 on chromosome Xq21.1 Contains putative purinergic receptor P2Y10 /cds=(0,1019) /gb=Z82200 /gi=2370075 /lug=Hs.166137 /len=1020  | 36413_at |
| IFI41 (interferon-induced protein 41, 30KD) | L22342   | Hs.241510 | NM_004509 |      | Cluster Incl. L22342:Human nuclear phosphoprotein mRNA, complete cds /cds=(0,746) /gb=L22342 /gi=402204 /lug=Hs.38125 /len=835  | 35718_at |
| ARH1 (ras homolog gene family, member H)    | Z35227   | Hs.109918 | NM_004310 | 4p13 | Cluster Incl. Z35227:H.sepiens TTF mRNA for small G protein /cds=(579,1154)   | 37416_at |

|   |          |          |           |         |   |  |           |
|---|----------|----------|-----------|---------|---|--|-----------|
|   |          |          |           |         |   | /gb=Z35227 /gj=609016 /ug=Hs.109918<br>/len=1427   |           |
| PRKCB1 (protein kinase C, beta 1)   | X07109   | Hs.77202 | NM_002738 | 16p11.2 | X07109  | /FEATURE=cds<br>/DEFINITION=HSPKCB2A Human mRNA<br>for protein kinase C (PKC) type beta II | 1217_g_at |
|   | AL049471 |          |           |         | Cluster Incl. AL049471:Homo sapiens<br>mRNA; cDNA DKFZp586N012 (from clone<br>DKFZp586N012) /cds=UNKNOWN<br>/gb=AL049471 /gj=4500266 /ug=Hs.12702<br>/len=2905  |  | 41690_at  |
| KCNN4 (potassium intermediate/small<br>conductance calcium-activated<br>channel, subfamily N, member 4) | AF022797 | Hs.10082 | NM_002250 | 19q13.2 | Cluster Incl. AF022797:Homo sapiens<br>intermediate conductance calcium-<br>activated potassium channel (hKCa4)<br>mRNA, complete cds /cds=(396,1679)<br>/gb=AF022797 /gj=2674355 /ug=Hs.10082<br>/len=2238 |  | 41106_at  |

|  |          |          |           |       |  |          |
|--|----------|----------|-----------|-------|--|----------|
| USF2 (upstream transcription factor 2, c-fos interacting)              | AD000684 | Hs.93649 | NM_003367 | 19q13 | Cluster Incl. AD000684:Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence /cds=(0,1290) /gb=AD000684 /gi=1905917 /ug=Hs.95697 /len=1291 | 38324_at |
| KIAA0471( KIAA0471 gene product )                                      | AB007940 |          |           | 1     | Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete cds /cds=(412,1524) /gb=AB007940 /gi=3413903 /ug=Hs.107325 /len=6834                             | 34445_at |
| SLC23A1 (solute carrier family 23 (nucleobase transporters), member 1) | D87075   | Hs.82042 | NM_005116 | 20p13 | Cluster Incl. D87075:Human mRNA for KIAA0238 gene, partial cds /cds=(0,992) /gb=D87075 /gi=1510150 /ug=Hs.82042 /len=5608  | 38122_at |
| KIAA0441( KIAA0441 gene product )                                      | AB007901 |          |           |       | Cluster Incl. AB007901:Homo sapiens KIAA0441 mRNA, complete cds /cds=(168,2261) /gb=AB007901 /gi=2662162 /ug=Hs.32511 /len=5597  | 39658_at |

|  |          |          |           |          |   |  |          |
|--|----------|----------|-----------|----------|---|--|----------|
|  |          |          |           |          | 6 | Cluster Incl. X07203:Human mRNA for CD20 receptor (S7) /cds=(90,983) /gb=X07203 /gi=29775 /ug=Hs.89751 /len=1597                                     | 40749_at |
| LEF1 (lymphoid enhancer-binding factor 1)      | AL049409 | Hs.44865 | NM_016269 | 4q23-q25 |   | Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419 | 36021_at |
| TCL1A (T-cell leukemia/lymphoma 1A)            | X82240   | Hs.2484  | NM_021966 | 14q32.1  |   | Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312                          | 39318_at |
| SCAP1 (src family associated phosphoprotein 1) | Y11215   | Hs.19126 | NM_003726 | 17q21.3  |   | Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524                               | 38862_at |

|   |          |           |           |          |  |          |
|---|----------|-----------|-----------|----------|--|----------|
| NCOA1 (nuclear receptor coactivator 1)                                      | U59302   | Hs.74002  | NM_003743 | 2p23     | U59302<br>/DEFINITION=HSU59302 Human steroid<br>receptor coactivator-1 F-SRC-1 mRNA,<br>complete cds                                 | 484_at   |
| TRAF1 (TNF receptor-associated factor 1)                                    | U19261   | Hs.2134   | NM_005658 | 9q33-q34 | U19261<br>/DEFINITION=HSU19261 Homo sapiens<br>Epstein-Barr virus-induced protein mRNA,<br>complete cds                              | 849_g_at |
| KIAA0239( KIAA0239 protein )  | D87076   | Hs.9729   | NM_015288 | 5        | Cluster Incl. D87076:Human mRNA for<br>KIAA0239 gene, partial cds /cds=(0,1716)<br>/gb=D87076 /gj=1510152 /ug=Hs.9729<br>/len=5630   | 38342_at |
| CASK (calcium/calmodulin-dependent serine<br>protein kinase (MAGUK family)) | AF035582 | Hs.151469 | NM_003888 | xp11.4   | Cluster Incl. AF035582:Homo sapiens<br>CASK mRNA, complete cds<br>/cds=(15,2708) /gb=AF035582<br>/gj=2661105 /ug=Hs.151469 /len=3919 | 31854_at |
| KIAA0053( KIAA0053 gene product )   | D29642   | Hs.1528   | NM_014882 | 2        | Cluster Incl. D29642:Human mRNA for<br>KIAA0053 gene, complete cds   | 38149_at |



|                               |          |           |           |         |   |  |  |  |  |
|-------------------------------|----------|-----------|-----------|---------|---|--|--|--|--|
|                               |          |           |           |         |   | /cds=(193,2109) /gb=D29642 /gi=473934<br>/ug=Hs.1528 /len=2739 |  |  |  |
| APOC4 (apolipoprotein C-IV)   | U32576   | Hs.110675 | NM_001646 | 19q13.2 | Cluster Incl. U32576:Human<br>apolipoprotein apoC-IV (APOC4) gene,<br>complete cds /cds=(40,423) /gb=U32576<br>/gi=975892 /ug=Hs.110675 /len=613  | 34454_r_at   |  |  |  |
| SP100 (nuclear antigen Sp100) | M60618   | Hs.77617  | NM_003113 | 2q37.1  | Cluster Incl. M60618:Human nuclear<br>autoantigen (SP-100) mRNA, complete<br>cds /cds=(31,1473) /gb=M60618<br>/gi=178888 /ug=Hs.77617 /len=1879   | 37352_at   |  |  |  |
| KIAA1010( KIAA1010 protein )  | AB023227 | Hs.23860  |           | 10      | Cluster Incl. AB023227:Homo sapiens<br>mRNA for KIAA1010 protein, partial cds<br>/cds=(0,3949) /gb=AB023227 /gi=4589669<br>/ug=Hs.23860 /len=5524 | 34712_at   |  |  |  |
| SP100 (nuclear antigen Sp100) | M60618   | Hs.77617  | NM_003113 | 2q37.1  | Cluster Incl. M60618:Human nuclear<br>autoantigen (SP-100) mRNA, complete<br>cds /cds=(31,1473) /gb=M60618  | 37353_g_at   |  |  |  |

|  |          |           |           |              |  |                                   |  |
|--|----------|-----------|-----------|--------------|--|-----------------------------------|--|
|  |          |           |           |              |  | /gi=178688 /ug=Hs.77617 /len=1879 |  |
| JAK1 (Janus kinase 1 (a protein tyrosine kinase))  | AL039831 | Hs.50651  | NM_002227 | 1p32.3-p31.3 | Cluster Incl. AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3' end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651 /len=579 | 34877_at                          |  |
| PPP3CC (protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)) | S46622   | Hs.75206  | NM_005605 | 8            | Cluster Incl. S46622:calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134   | 32541_at                          |  |
| MTMR1 (myotubularin related protein 1)   | AJ224979 | Hs.23200  |           | xq28         | Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200 /len=2582                           | 34654_at                          |  |
| HLA-F (major histocompatibility complex, class I, F)   | AL022723 | Hs.110309 | NM_018950 | 6p21.3       | Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723                               | 37420_i_at                        |  |

|  |          |           |           |               |  |   |           |  |  |  |
|--|----------|-----------|-----------|---------------|--|---|-----------|--|--|--|
|  |          |           |           |               |  | /gi=5002624 /ug=Hs.110309 /len=1303   |           |  |  |  |
| PRKCB1 (protein kinase C, beta 1)  | X06318   | Hs.77202  | NM_002738 | 16p11.2       | X06318   | /FEATURE=cds<br>/DEFINITION=HSPKCB1A Human mRNA<br>for protein kinase C (PKC) type beta I | 1336_s_at |  |  |  |
| GTSE1 (G-2 and S-phase expressed 1)  | AL031588 | Hs.122552 | NM_016426 | 22q13.2-q13.3 | Cluster Incl. AL031588.dJ1163J1.3 (novel<br>protein similar to mouse B99)<br>/cds=(0,2140) /gb=AL031588 /gi=4007108<br>/ug=Hs.122552 /len=2821 |   | 39872_at  |  |  |  |
| SLC7A6 (solute carrier family 7 (cationic amino<br>acid transporter, y+ system), member 6) | D87432   | Hs.10315  | NM_003983 | 16q22.1-q22.3 | Cluster Incl. D87432:Human mRNA for<br>KIAA0245 gene, complete cds<br>/cds=(261,1806) /gb=D87432 /gi=1665758<br>/ug=Hs.10315 /len=6296         |   | 39533_at  |  |  |  |

Table 16: Major Types (BM, CLL, CML, ALL, AML)

## HAUPTGRUPPEN

| COMPARISON |          | Description  |                                      |  |        |             |
|------------|----------|--|--------------------------------------|--|--------|-------------|
| CLL - CML  |          | M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA complete cds  | HG_U95_Target: 1105_s_at_HG- U95Av2  | T cell receptor beta locus             | TRB    | 7q35        |
| AML - CML  |          | Cluster Incl. AL036554:DKFZp564J2262_1 Homo sapiens cDNA 5' end; clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.137931793 /len=517 | HG_U95_Target: 31793_at_HG- U95Av2   | defensin, alpha 3, neutrophil-specific | DEFA3  | 8pter-p23.3 |
| AML - BM   | ALL - BM | Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510298 /ug=Hs.198282 /len=2077                     | HG_U95_Target: 32775_r_at_HG- U95Av2 | phospholipid scramblase 1              | PLSCR1 | 3q23        |

|           |  |   |  |           |          |
|-----------|--|---|--|-----------|----------|
| AML - CML | Cluster Incl. A1762213:wi54d04.x1 Homo sapiens cDNA, 3' end /cds=IMAGE2394055 /cds_end=3 /gb=A1762213 /gi=5177880 /ug=Hs.204238 /len=677                             | HG_U95_Target<br>32821_at_HG-<br>U95AV2 | lipocalin 2 (oncogene 24p3)                | LCN2      | 9q34     |
| ALL - BM  | Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150                            | HG_U95_Target<br>33860_at_HG-<br>U95AV2 | KIAA0462 protein                           | KIAA0462* | 1p36.13  |
| ALL - AML | Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.6479733944_at_HG- /len=3727 | HG_U95_Target<br>33944_at_HG-<br>U95AV2 | amyloid beta (A4) precursor-like protein 2 | APLP2     | 11q24    |
| ALL - AML | Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586i0919 (from clone DKFZp586i0919) /cds=UNKNOWN /gb=AL049409 /gi=450019436021_at_HG- /ug=Hs.44865 /len=1419     | HG_U95_Target<br>36021_at_HG-<br>U95AV2 | lymphoid enhancer-binding factor 1         | LEF1      | 4q23-q25 |
| AML - CLL | Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301   | HG_U95_Target<br>36239_at_HG-<br>U95AV2 | POU domain, class 2, associating factor 1  | POU2AF1   | 11q23.1  |
| AML - CML | Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213812 /ug=Hs.54431 /len=2124  | HG_U95_Target<br>36464_at_HG-<br>U95AV2 | specific granule protein (28 kDa)          | SGP28*    | 6p12.3   |

|           |  |  |  |          |                                  |        |               |
|-----------|--|--|--|----------|----------------------------------|--------|---------------|
|           |  |  | U95AV2                                   |          |                                  |        |               |
| ANIL - BM |  | Cluster Incl. Z38026: H.sapiens mRNA for FALL-39 peptide antibiotic<br>(cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615   | HG_U95_Target:<br>36710_at_HG-<br>U95AV2 | 36710_at | cathelidin antimicrobial peptide | CAMP   | 3p21.3        |
| ALL - CML |  | Cluster Incl. L01664: Human eosinophil Charcot-Leyden crystal (CLC) protein<br>(lysophospholipase) mRNA, complete cds (cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586                                | HG_U95_Target:<br>36809_at_HG-<br>U95AV2 | 36809_at | Charot-Leyden crystal protein    | CLC    | 19q13.1       |
| ALL - AML |  | Cluster Incl. U41635: Human OS-9 precursor mRNA, complete cds<br>(cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736  | HG_U95_Target:<br>36996_at_HG-<br>U95AV2 | 36996_at | amplified in osteosarcoma        | OS-9*  | 12q13         |
| ALL - CML |  | Cluster Incl. AF010400: untitled (cds=(50,1063) /gb=AF010400 /gi=2612876<br>/ug=Hs.77290 /len=1242   | HG_U95_Target:<br>37311_at_HG-<br>U95AV2 | 37311_at | transaldolase 1                  | TALDO1 | 11p15.5-p15.4 |
| BM - CML  |  | Cluster Incl. U52682: Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds<br>(cds=(125,1477) /gb=U52682 /gi=1376108 /ug=Hs.82132 /len=5320 | HG_U95_Target:<br>37625_at_HG-<br>U95AV2 | 37625_at | Interferon regulatory factor 4   | IRF4   | 6p25-p23      |

|           |   |  |          |  |          |          |
|-----------|---|--|----------|--|----------|----------|
| BM - CLL  | Cluster Incl. AB023169: Homo sapiens mRNA for KIAA0952 protein, complete cds<br>(cds=(359,1927) /gb=AB023169 /gi=4589547 /ug=Hs.7935 /len=4856  | HG_U95_Target:<br>37755_at_HG-<br>U95AV2 | 37755_at | KIAA0952 protein   | KIAA0952 | 20p12.1  |
| ALL - CLL | Cluster Incl. U92981: Homo sapiens clone DT1P186 mRNA, CAG repeat region<br>(cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429  | HG_U95_Target:<br>38577_at_HG-<br>U95AV2 | 38577_at | unknown  | Unknown* | unknown  |
| AML - CLL | Cluster Incl. M63928: Homo sapiens T cell activation antigen (CD27) mRNA, complete cds (cds=(100,862) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204   | HG_U95_Target:<br>38578_at_HG-<br>U95AV2 | 38578_at | tumor necrosis factor receptor superfamily, member 7                 | TNFRSF7  | 12p13    |
| ALL - BM  | Cluster Incl. U04270: Human putative potassium channel subunit (h-erg) mRNA, complete cds (cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.18802 /len=4070  | HG_U95_Target:<br>38858_at_HG-<br>U95AV2 | 38858_at | potassium voltage-gated channel, subfamily H (eag-related), member 2 | KCNH2    | 7q35-q38 |
| ALL - AML | Cluster Incl. AL008726.dJ337O18.2 (Lysosomal Protective Protein precursor (ECH3.4.18.5, Cathepsin A, Carboxypeptidase C)) (cds=(133,1575) /gb=AL00872639062 /gi=3183870 /ug=Hs.118126 /len=1946 | HG_U95_Target:<br>39062_at_HG-<br>U95AV2 | 39062_at | protective protein for beta-galactosidase (galactosialdosis)         | PPGB     | 20q13.1  |
| BM - CLL  | Cluster Incl. U03057: Human actin bundling protein (HSN) mRNA, complete cds (cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767   | HG_U95_Target:<br>39070_at_HG-           | 39070_at | singed (Drosophila)-like (sea urchin fascin homolog like)            | SNL      | 7p22     |

|           |          |  |  |                 |  |                |              |  |
|-----------|----------|--|--|-----------------|--|----------------|--------------|--|
|           |          |  | U95AV2                                   |                 |  |                |              |  |
| ALL - AML |          | Cluster Incl. AB023208: Homo sapiens mRNA for KIAA0991 protein, complete cds<br>/cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938 | HG_U95_Target:<br>41220_at_HG-<br>U95AV2 | 41220_at        | MLL septin-like fusion                                 | MSF            | 17q25        |  |
| CLL - CML | BM - CML | Cluster Incl. U15085: Human HLA-DMB mRNA, complete cds /cds=(233,1024)<br>/gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362                            | HG_U95_Target:<br>41609_at_HG-<br>U95AV2 | 41609_at        | major histocompatibility<br>complex, class II, DM beta | HLA-DMB        | 6p21.3       |  |
| ALL - CLL |          | U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor<br>coactivator-1 F-SRC-1 mRNA, complete cds   | HG_U95_Target:<br>484_at_HG-<br>U95AV2   | 484_at          | nuclear receptor coactivator 1                         | NCOA1          | 2p23         |  |
|           |          | description  | HG-U95_Target                            | Probe Set<br>ID | Title  | Gene<br>Symbol | Map Location |  |



Table 17. AML\_WHO [other, t(11q23)/MLL, t(8;21), inv(16), t(15;17)]

|             |             |            |  |                                    |            |   |       |                 |
|-------------|-------------|------------|--|------------------------------------|------------|---|-------|-----------------|
| INV16-      | INV16-OTHER | INV16-T821 | Cluster Incl. AF013570: Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580 | HG_U85_Target:37407_s_at_HG-U85AV2 | 37407_s_at | myosin, heavy polypeptide 11, smooth muscle | MYH11 | 16p13.13-p13.12 |
| INV16-      |             |            | AF001548 /FEATURE=mRNA /DEFINITION=HUA01548 Human Chromosome 16 BAC clone C1987SK-A1_HG-U85AV2 815A9, complete sequence  | HG_U85_Target:787_s_at_HG-U85AV2   | 787_at     | myosin, heavy polypeptide 11, smooth muscle | MYH11 | 16p13.13-p13.12 |
| INV16-OTHER |             |            | Cluster Incl. U68186: Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660883 /ug=Hs.81071 /len=1819                                      | HG_U85_Target:37600_s_at_HG-U85AV2 | 37600_at   | extracellular matrix protein 1              | ECM1  | 1q21            |

|             |          |  |  |  |   |                                  |          |  |          |          |
|-------------|----------|--|--|--|---|----------------------------------|----------|--|----------|----------|
| INV16-T1517 |          |  |  |  | M25280<br>/DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds   | HG_U95_Target:245_at_HG-U95AV2   | 245_at   | selectin L (lymphocyte adhesion molecule 1)            | SELL     | 1q23-q25 |
| INV16-T1517 |          |  |  |  | Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain<br>/cds=(0,702) /gb=X00457 /gl=36405<br>/ug=Hs.914 /len=1048                  | HG_U95_Target:38833_at_HG-U95AV2 | 38833_at | major histocompatibility complex, class II, DP alpha 1 | HLA-DPA1 | 6p21.3   |
| INV16-T821  |          |  |  |  | Cluster Incl. AF008484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,869) /gb=AF008484 /gl=2738496 /ug=Hs.3436 /len=1608 | HG_U95_Target:41535_at_HG-U95AV2 | 41535_at | CDK2-associated protein 1                              | CDK2AP1  | 12q24.31 |
| MLL-        |          |  |  |  | Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1414,2526) /gb=AB007888 /ug=Hs.28578 /len=5940  | HG_U95_Target:34306_at_HG-U95AV2 | 34306_at | muscleblind (Drosophila)-like                          | MBNL     | 3q25     |
| MLL-        | MLL-T821 |  |  |  | Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein beta subunit<br>/cds=(27,794) /gb=X71129 /gl=297901  | HG_U95_Target:36881_at_HG-U95AV2 | 36881_at | electron-transfer-flavoprotein, beta polypeptide       | ETFB     | 19q13.3  |

[illegible]

|           |             |        |            |  |          |  |         |          |
|-----------|-------------|--------|------------|--|----------|--|---------|----------|
| MLL-OTHER |             |        |            | Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,1095) /hg_U95_Target:36980 /gb=U03105 /gi=476094 /ug=Hs.75969_at_HG-U95AV2 /len=2061  | 36980_at | proline-rich protein with nuclear targeting signal | B4-2*   | 6q16.1   |
| MLL-OTHER |             |        |            | Cluster Incl. AF001461: Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA, complete cds /cds=(30,881) /gb=AF001461 /gi=3378030 /ug=Hs.76526 /len=1354 | 37026_at | core promoter element binding protein              | COPEB   | 10p15    |
| MLL-OTHER |             |        |            | Cluster Incl. M36542: Human lymphoid-specific transcription factor mRNA, complete cds /cds=(54,1445) /gb=M36542 /gi=339495 /ug=Hs.1101 /len=2048           | 37417_at | POU domain, class 2, transcription factor 2        | POU2F2  | 19q13.31 |
| MLL-T1517 |             |        |            | Cluster Incl. U25182: Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921                        | 38435_at | peroxiredoxin 4                                    | PRDX4   | Xp22.13  |
| MLL-T1517 | OTHER-T1517 | T1517- | T1517-T821 | Cluster Incl. X78817: Homo sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817   | 39849_at | Rho GTPase activating protein 4                    | ARHGAP4 | Xq28     |



|                    |  |  |  |  |               |   |             |              |
|--------------------|--|--|--|--|---------------|---|-------------|--------------|
| T1517-             |  |  |  | Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /HG_U85_Target:38487 /gb=D87433 /gl=1665760 /ug=Hs.84753_at_HG-U85AV2 /len=6777                   | 38487_at      | hypothetical protein FLJ12442, KIAA0246   | STAB1*      | 3p21.31      |
| T821-              |  |  |  | Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA /HG_U85_Target:33121 /cds=(132,635) /gb=AF045229_g_at_HG-U85AV2 /gl=2806028 /ug=Hs.82280 /len=753 | 33121_g_at    | regulator of G-protein signalling 10  | RGS10       | 10q25        |
| T821-              |  |  |  | Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /HG_U85_Target:35638 /cds=(411,2144) /gb=D43638 /gl=940399_at_HG-U85AV2 /ug=Hs.31551 /len=3460                 | 35638_at      | core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related | CBFA2T1     | 8q22         |
| T821-              |  |  |  | Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /HG_U85_Target:35940 /cds=(277,1272) /gb=X64624 /gl=35914_at_HG-U85AV2 /ug=Hs.211588 /len=3492     | 35940_at      | POU domain, class 4, transcription factor 1   | POU4F1      | 13q21.1-q22  |
| used in comparison |  |  |  | Description  | HG-U85 Target | Title   | Gene Symbol | Map Location |

Table 17. Hierarchical clustering of 55 AML samples (rows) versus 25 informative genes (columns). In total, 15 comparisons within the 5 groups were performed (pairwise and one-versus-all). Genes were selected for maximal accuracy and confidence based on a modified signal-to-noise (S2N) algorithm [see (Ref)]. The scaled gene expression levels are coded by intensity and shown on a scale from black (no gene expression) to bright red (highest expression). The AML subgroups 'other' (n=10), t(11q23)/MLL (n=10), inv(16) (n=10), t(8;21) (n=9), and t(15;17) (n=16) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by approved symbols by the HGNC (not yet approved genes are marked by asterisks).

Table 18. ALL\_détail [t(11q23)/MLL, t(9;22), t(8;14), T-ALL]

|               |  |                                   |           |  |     |              |
|---------------|--|-----------------------------------|-----------|--|-----|--------------|
| ALLPH-ALLT    | M12888 /FEATURE= /DEFINITION=HUMTCBY Human T-cell receptor active beta-chain mRNA, complete cds                                  | HG_U95_Target:1105_s_at_HG-U95AV2 | 1105_s_at | T cell receptor beta locus   | TRB | 7q35         |
| ALLPH-        | U03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblastic leukemia antigen (CALLA) mRNA, complete cds           | HG_U95_Target:1389_s_at_HG-U95AV2 | 1389_at   | membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) | MME | 3q25.1-q25.2 |
| ALL814-       | M16038 /FEATURE= /DEFINITION=HUMLYN Human lymphoma tyrosine kinase mRNA encoding a tyrosine kinase                               | HG_U95_Target:1402_s_at_HG-U95AV2 | 1402_at   | v-src-1 Yamaguchi sarcoma viral related oncogene homolog                           | LYN | 8q13         |
| ALL814-ALLMLL | U22376 /FEATURE=cds#3 /DEFINITION=HSU22376 Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds | HG_U95_Target:1474_s_at_HG-U95AV2 | 1474_s_at | v-myb myeloblastosis viral oncogene homolog (avian)                                | MYB | 6q22-q23     |
| ALL814-ALLMLL | M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA, complete cds  | HG_U95_Target:2042_s_at_HG-U95AV2 | 2042_s_at | v-myb avian myeloblastosis viral oncogene homolog                                  | MYB | 6q22-q23     |



|              |  |                                      |           |  |         |           |
|--------------|--|--------------------------------------|-----------|--|---------|-----------|
| ALLMLL-ALLT  | 123805 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin mRNA, complete cds   | HG_U95_Target:2069<br>s_at_HG-U95AV2 | 2069_s_at | catenin (cadherin-associated protein), alpha 1<br>(102kD)                  | CTNNA1  | 5q31      |
| ALLT-        | Cluster Incl. AL034374:Human DNA sequence from clone 4B3K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL034374 /gi=44555665 /ug=Hs.234655 /len=2432 | HG_U95_Target:3382<br>s_at_HG-U95AV2 | 3382_s_at | homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2 | HELO1   | 6         |
| ALL814-ALLPH | Cluster Incl. AB020674:Homo sapiens mRNA for KIAA0867 protein, complete cds /cds=(152,1732) /gb=AB020674 /gi=4240222 /ug=Hs.52081 /len=4339  | HG_U95_Target:3526<br>s_at_HG-U95AV2 | 3526_s_at | KIAA0867 protein   | MONDOA* | 12q21.31  |
| ALL814-ALLT  | Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, complete cds /cds=(86,364) /gb=D90144 /gi=219905 /ug=Hs.73817 /len=781  | HG_U95_Target:3610<br>s_at_HG-U95AV2 | 3610_s_at | small inducible cytokine A3 (homologous to mouse Mip-1a)                   | SCYA3   | 17q11-q21 |
| ALLMLL-      | Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312   | HG_U95_Target:3663<br>s_at_HG-U95AV2 | 3663_s_at | connective tissue growth factor  | CTGF    | 6q23.1    |

|              |       |   |  |            |  |           |          |
|--------------|-------|---|--|------------|--|-----------|----------|
| ALLMLL-      |       | Cluster Incl. D16532:Human gene for very low density lipoprotein receptor, 5flanking and /cds=(615,3236) /gb=D16532 /gl=407220 /ug=Hs.73728 /len=3853 | HG_U95_Target:3687<br>3_at_HG-U95AV2   | 36873_at   | very low density lipoprotein receptor                  | VLDLR     | 9p24     |
| ALL814-      |       | Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gl=2182176 /ug=Hs.78274 /len=1597  | HG_U95_Target:3774<br>7_at_HG-U95AV2   | 37747_at   | annexin A5   | ANXA5     | 4q28-q32 |
| ALLPH-ALLT   | ALLT- | Cluster Incl. AA919102:cl84h02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gl=3058992 /ug=Hs.95327 /len=622          | HG_U95_Target:3831<br>9_at_HG-U95AV2   | 38319_at   | CD3D antigen, delta polypeptide (T13 complex)          | CD3D      | 11q23    |
| ALLMLL-ALLPH |       | Cluster Incl. AJ010059:Homo sapiens . SIT protein /cds=(87,677) /gb=AJ010059 /gl=4888891 /ug=Hs.88012 /len=1232                                       | HG_U95_Target:4072<br>3_at_HG-U95AV2   | 40723_at   | SHP2 interacting transmembrane adaptor                 | SIT*      | 9p13-p12 |
| ALLMLL-ALLT  |       | Cluster Incl. AF-102803:untitled /cds=(2,2722) /gb=AF-102803 /gl=4092760 /ug=Hs.178452 /len=3668  | HG_U95_Target:4115<br>3_f_at_HG-U95AV2 | 41153_f_at | catenin (cadherin-associated protein), alpha 1 (102KD) | CTNNA1    | 5q31     |
| ALL814-ALLPH |       | Cluster Incl. AW024285:w659d06.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2512715 /clone_end=3 /gb=AW024285 /gl=5877815 /ug=Hs.179882 /len=550         | HG_U95_Target:4117<br>7_at_HG-U95AV2   | 41177_at   | hypothetical protein FLJ12443                          | FLJ12443* | 5p15.33  |

|                    |  |                                |                               |             |              |
|--------------------|--|--------------------------------|-------------------------------|-------------|--------------|
| ALLB14-ALLT        | Cluster Incl. X02894:Human mRNA for adenosine deaminase (adenosine aminohydrolyase, EC 3.5.4.4) /gb=X02894 /gi=28379 /ug=Hs.12174_at_HG-U95AV2 /len=1498 | HG_U95_Target:4155<br>41854_at | adenosine deaminase           | ADA         | 20q12-q13.11 |
| ALLPH-             | Cluster Incl. AB020677: Homo sapiens mRNA for KIAA0870 protein, complete cds /cds=(436,1998) /gb=AB020677 /gi=4240228 /ug=Hs.18166 /len=4484             | HG_U95_Target:4173<br>41734_at | KIAA0870 protein              | KIAA0870*   | 8q24.3       |
| ALLMIL-ALLPH       | Glucocorticoid Receptor, Beta  | HG_U95_Target:706<br>706_at    | Glucocorticoid Receptor, Beta |             |              |
| used in comparison | Description_Affymetrix   | HG-U95 Target                  | Title                         | Gene Symbol | Map Location |

**Table 18.** Hierarchical clustering of 17 ALL samples (rows) versus 19 informative genes (columns). In total, 10 pairwise or OVA comparisons within the 4 groups were performed. Genes were selected for maximal accuracy and confidence based on a modified

S2N algorithm [see (Ref)]. The scaled gene expression levels are coded by intensity and shown on a scale from black (no gene expression) to bright red (highest expression). The ALL subgroups t(11q23)/MLL (n=4), t(9;22) (n=7), t(8;14) (n=3), and T-ALL (n=3) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by approved symbols by the HGNC (asterisks mark not yet approved genes).

Table 19 - Additional Comparisons

| ALLPHNEG - ALLPHPOS |  |                                  |          |                     |          |          |  |
|---------------------|--|----------------------------------|----------|---------------------|----------|----------|--|
| 38336_at            | Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial cds /cds=(0,3188) /gb=AB023230 /gi=4588675 /ug=Hs.96427 /len=4783 | HG_U95_Target:38336_at_HG-U95AV2 | 38336_at | KIAA1013 protein    | KIAA1013 | 3        |  |
| 33134_at            | Cluster Incl. AB011083:Homo sapiens mRNA for KIAA0511 protein, partial cds /cds=(0,2802) /gb=AB011083 /gi=3043545 /ug=Hs.8402 /len=3563  | HG_U95_Target:33134_at_HG-U95AV2 | 33134_at | adenylate cyclase 3 | ADCY3    | 2p24-p22 |  |

|             |  |                                  |          |  |      |       |  |
|-------------|--|----------------------------------|----------|--|------|-------|--|
| ALLB - ALLT |  |                                  |          |  |      |       |  |
| 38319_at    | Cluster Incl. AA919102:cl94h02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622 | HG_U95_Target:38319_at_HG-U95AV2 | 38319_at | CD3D antigen, delta polypeptide (TIT3 complex) | CD3D | 11q23 |  |

|             |  |  |   |          |               |
|-------------|--|--|---|----------|---------------|
| 1105_s_at   | M12886 /FEATURE= /DEFINITION=HUMTCBYH<br>Human T-cell receptor active beta-chain mRNA,<br>complete cds   | HG_U95_Target:1105_s_1105_s_at<br>at_HG-U95AV2 | T cell receptor beta locus  | TRB      | 7q35          |
| ALLPH - CML |  |  |   |          |               |
| 38894_g_at  | Cluster Incl. AL008637:Human DNA sequence from<br>clone 833B7 on chromosome 22q12.3-13.2 Contains<br>genes for NCF4 (P40PHOX) protein, cytokine receptor<br>common beta chain precursor CSF2RB (partial)<br>ESTs, CA repeat, STS, GSS /cds=(629,1648)<br>/gb=AL008637 /gl=3136 | HG_U95_Target:38894_38894_g_at<br>at_HG-U95AV2 | Cluster   | AL008637 | unknown       |
| 35016_at    | Cluster Incl. M13560:Human Ia-associated invariant<br>gamma-chain gene /cds=(795,1493) /gb=M13560<br>/gl=184518 /ug=Hs.84298 /len=2080   | HG_U95_Target:35016_35016_at<br>at_HG-U95AV2   | CD74 antigen (invariant polypeptide of major<br>histocompatibility class II antigen-associated) | CD74     | 5q32          |
| 39301_at    | Cluster Incl. X85030:Human spleen mRNA for skeletal<br>muscle-specific calpain /cds=(0,2465) /gb=X85030<br>/gl=791039 /ug=Hs.239689 /len=2466  | HG_U95_Target:39301_39301_at<br>at_HG-U95AV2   | calpain 3, (p94)  | CAPN3    | 15q15.1-q21.1 |

|                 |   |                                  |          |  |      |        |  |
|-----------------|---|----------------------------------|----------|--|------|--------|--|
| ALLMLL - AMLMLL |   |                                  |          |  |      |        |  |
| 266_s_at        | L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA complete cds and 3' region                           | HG_U95_Target:266_s_at_HG-U95AV2 | 266_s_at | CD24 antigen (small cell lung carcinoma cluster 4 antigen) | CD24 | 6q21   |  |
| 36638_at        | Cluster Ind. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gj=474933 /ug=Hs.75511 /len=2312 | HG_U95_Target:36638_at_HG-U95AV2 | 36638_at | connective tissue growth factor                            | CTGF | 6q23.1 |  |

WO 03/039443

656

PCT/EP02/12303



Table 20

**1. Analyse: major leukemia types versus normal bone marrow**

| ALL - AML         |            | samples: 18 / 59  | pValue | selected |
|-------------------|------------|-------------------|--------|----------|
| <i>accuracy</i>   |            | 0.974025974025974 |        |          |
| <i>confidence</i> |            | 0.949191799863432 |        |          |
| 1                 | 41220_at   | 1.43161207339479  | 0      | *        |
| 2                 | 36996_at   | -1.41523985920205 | 0      | *        |
| 3                 | 33944_at   | -1.36856428236618 | 0      | *        |
| 4                 | 41809_at   | 1.34726978852919  | 0      |          |
| 5                 | 39062_at   | -1.32477468024042 | 0      | *        |
| 6                 | 36021_at   | 1.29482788383042  | 0      | *        |
| 7                 | 40282_s_at | -1.25276275727203 | 0      |          |
| 8                 | 39801_at   | -1.18216117554755 | 0      |          |
| 9                 | 41808_at   | 1.16535104461878  | 0      |          |
| 10                | 38791_at   | -1.16212420300011 | 0      |          |

|    |          |                   |   |
|----|----------|-------------------|---|
| 11 | 38705_at | 1.10578452683281  | 0 |
| 12 | 38017_at | 1.09519463190211  | 0 |
| 13 | 38233_at | -1.08734958364712 | 0 |
| 14 | 40081_at | -1.06895950257537 | 0 |
| 15 | 33414_at | -1.06893939139052 | 0 |
| 16 | 36644_at | -1.06866972901421 | 0 |
| 17 | 1497_at  | -1.05371604908866 | 0 |
| 18 | 34670_at | -1.0471297974693  | 0 |
| 19 | 39689_at | -1.02349800799274 | 0 |
| 20 | 36553_at | 0.461827371901751 | 0 |

ALL - BM

samples: 18 / 8

*accuracy*

1

*confidence*

0.973577941615687

|   |            |                   |   |   |
|---|------------|-------------------|---|---|
| 1 | 32775_r_at | -1.99123472883631 | 0 | * |
| 2 | 38858_at   | -1.89835994048167 | 0 | * |
| 3 | 33860_at   | -1.8349786493313  | 0 | * |
| 4 | 33944_at   | -1.79527299060519 | 0 |   |

|    |            |                   |   |
|----|------------|-------------------|---|
| 5  | 32800_at   | -1.78206927960542 | 0 |
| 6  | 35204_at   | -1.77698316964481 | 0 |
| 7  | 38112_g_at | -1.75527325798005 | 0 |
| 8  | 38735_at   | -1.75431905717345 | 0 |
| 9  | 137_at     | -1.75261998994426 | 0 |
| 10 | 1495_at    | -1.73006006400362 | 0 |
| 11 | 36661_s_at | -1.70636382014738 | 0 |
| 12 | 38225_at   | -1.66016477586249 | 0 |
| 13 | 39860_at   | 1.65854625573936  | 0 |
| 14 | 32166_at   | -1.65691236756089 | 0 |
| 15 | 32530_at   | 1.64232673980553  | 0 |
| 16 | 35355_at   | 1.62316234982832  | 0 |
| 17 | 1529_at    | -1.60938224689727 | 0 |
| 18 | 36790_at   | -1.6093508135706  | 0 |
| 19 | 2045_s_at  | -1.59880026139776 | 0 |
| 20 | 36553_at   | 0.997704664996536 | 0 |

ALL - CLL

samples: 18 / 8

|    |                   |                   |   |
|----|-------------------|-------------------|---|
|    | <i>accuracy</i>   | 1                 |   |
|    | <i>confidence</i> | 1                 |   |
| 1  | 484_at            | -2.96991037890552 | 0 |
| 2  | 38577_at          | -2.76720679743789 | 0 |
| 3  | 2019_s_at         | -2.66997144118244 | 0 |
| 4  | 33812_at          | -2.65004620998946 | 0 |
| 5  | 34663_at          | -2.56576070575816 | 0 |
| 6  | 36894_at          | -2.56382539311197 | 0 |
| 7  | 39670_at          | -2.48013356223836 | 0 |
| 8  | 41660_at          | -2.4799018378336  | 0 |
| 9  | 39165_at          | -2.3871739157192  | 0 |
| 10 | 31870_at          | -2.36838597731039 | 0 |
| 11 | 34871_at          | -2.36033294682702 | 0 |
| 12 | 34830_at          | -2.33471776306134 | 0 |
| 13 | 31936_s_at        | -2.25951360532653 | 0 |
| 14 | 1062_g_at         | -2.25550068155602 | 0 |
| 15 | 41847_at          | -2.23298915825072 | 0 |
| 16 | 1217_g_at         | -2.21920314115838 | 0 |

|    |          |                   |   |
|----|----------|-------------------|---|
| 17 | 1529_at  | -2.17991363072808 | 0 |
| 18 | 41796_at | -2.17392867117507 | 0 |
| 19 | 32597_at | -2.13552223797253 | 0 |
| 20 | 33266_at | 1.44232706973843  | 0 |

## ALL - CML

samples: 18 / 10

*accuracy*

1

*confidence*

1

|    |            |                   |   |   |
|----|------------|-------------------|---|---|
| 1  | 36809_at   | -2.79788870256583 | 0 | * |
| 2  | 37311_at   | -2.20009414203519 | 0 | * |
| 3  | 36766_at   | -2.15356495523503 | 0 |   |
| 4  | 38894_g_at | -2.11314073543331 | 0 |   |
| 5  | 39179_at   | -2.08890598787237 | 0 |   |
| 6  | 38893_at   | -2.05723533682216 | 0 |   |
| 7  | 37897_s_at | -2.05026870146261 | 0 |   |
| 8  | 41809_at   | 1.98458593845403  | 0 |   |
| 9  | 36963_at   | -1.95232400595449 | 0 |   |
| 10 | 39301_at   | -1.91549367394028 | 0 |   |

|    |            |                   |   |
|----|------------|-------------------|---|
| 11 | 40610_at   | 1.91246286924336  | 0 |
| 12 | 38879_at   | -1.87541355348469 | 0 |
| 13 | 41338_at   | 1.86506063801814  | 0 |
| 14 | 39968_at   | -1.81415292791782 | 0 |
| 15 | 33371_s_at | -1.81111388769192 | 0 |
| 16 | 37149_s_at | -1.77170759525375 | 0 |
| 17 | 38895_i_at | -1.77027078711718 | 0 |
| 18 | 41220_at   | 1.75387842844952  | 0 |
| 19 | 37099_at   | -1.74839569592051 | 0 |
| 20 | 40159_r_at | -1.35163593608562 | 0 |

AML - BM

samples: 59 / 8

*accuracy*

1

*confidence*

0.995997161972555

|   |            |                   |   |   |
|---|------------|-------------------|---|---|
| 1 | 36710_at   | -2.29217042550277 | 0 | * |
| 2 | 32775_r_at | -2.24397275344625 | 0 | * |
| 3 | 32821_at   | -1.98392215005915 | 0 |   |
| 4 | 37149_s_at | -1.94686927462724 | 0 |   |

|    |           |                   |   |
|----|-----------|-------------------|---|
| 5  | 37015_at  | -1.89128914250756 | 0 |
| 6  | 36894_at  | -1.80507021485339 | 0 |
| 7  | 38735_at  | -1.78884482794867 | 0 |
| 8  | 33752_at  | -1.77319451495748 | 0 |
| 9  | 34654_at  | -1.67560279229506 | 0 |
| 10 | 1115_at   | -1.62050106692579 | 0 |
| 11 | 31859_at  | -1.52416410078922 | 0 |
| 12 | 1980_s_at | 1.51765867172316  | 0 |
| 13 | 36464_at  | -1.49540428238676 | 0 |
| 14 | 38858_at  | -1.48511074361835 | 0 |
| 15 | 38225_at  | -1.4790110074487  | 0 |
| 16 | 39170_at  | -1.45392862675606 | 0 |
| 17 | 39929_at  | -1.44420537588163 | 0 |
| 18 | 36021_at  | -1.42322337311917 | 0 |
| 19 | 32259_at  | -1.41395952112425 | 0 |
| 20 | 41138_at  | 1.25347154740786  | 0 |

AML - CLL

samples: 59 / 8

|    |                   |                   |   |   |
|----|-------------------|-------------------|---|---|
|    | <i>accuracy</i>   | 1                 |   |   |
|    | <i>confidence</i> | 1                 |   |   |
| 1  | 36239_at          | -3.31028543322741 | 0 | * |
| 2  | 41220_at          | -3.2480863078754  | 0 |   |
| 3  | 1096_g_at         | -3.1269759462136  | 0 |   |
| 4  | 36155_at          | -3.08191178811872 | 0 |   |
| 5  | 38578_at          | -3.06174627261543 | 0 | * |
| 6  | 34871_at          | -3.02230826662657 | 0 |   |
| 7  | 38006_at          | -2.88939117591885 | 0 |   |
| 8  | 41165_g_at        | -2.87065891259428 | 0 |   |
| 9  | 1105_s_at         | -2.81674515012354 | 0 |   |
| 10 | 41166_at          | -2.75359060509193 | 0 |   |
| 11 | 31936_s_at        | -2.75277577570011 | 0 |   |
| 12 | 33812_at          | -2.74332185979714 | 0 |   |
| 13 | 41796_at          | -2.71763998725163 | 0 |   |
| 14 | 36894_at          | -2.64049311405919 | 0 |   |
| 15 | 38577_at          | -2.63072228466709 | 0 |   |
| 16 | 38666_at          | -2.61485585331331 | 0 |   |



|    |          |                   |   |
|----|----------|-------------------|---|
| 17 | 32597_at | -2.61456952032068 | 0 |
| 18 | 41847_at | -2.59409998700552 | 0 |
| 19 | 34830_at | -2.5698161906968  | 0 |
| 20 | 33266_at | 1.336807541194    | 0 |

## AML - CML

samples: 59 / 10

*accuracy*

1

*confidence*

0.956293899622379

|    |            |                   |   |   |
|----|------------|-------------------|---|---|
| 1  | 36464_at   | -2.85754269919935 | 0 | * |
| 2  | 32821_at   | -2.55228282645443 | 0 | * |
| 3  | 31859_at   | -2.27761090295808 | 0 |   |
| 4  | 37149_s_at | -2.11494842606363 | 0 |   |
| 5  | 36710_at   | -1.94749857224656 | 0 |   |
| 6  | 34546_at   | -1.85596431666606 | 0 |   |
| 7  | 33530_at   | -1.82614283985583 | 0 |   |
| 8  | 35919_at   | -1.74217437339032 | 0 |   |
| 9  | 37099_at   | -1.7184463713752  | 0 |   |
| 10 | 36165_at   | 1.7091639497163   | 0 |   |

|    |            |                    |     |
|----|------------|--------------------|-----|
| 11 | 37054_at   | -1.69705232668157  | 0   |
| 12 | 31381_at   | -1.6873086898061   | 0   |
| 13 | 37579_at   | -1.68217107035442  | 0   |
| 14 | 33371_s_at | -1.67508882502583  | 0   |
| 15 | 1117_at    | -1.67009743506797  | 0   |
| 16 | 38894_g_at | -1.66951302748224  | 0   |
| 17 | 31793_at   | -1.63477764661912  | 0 * |
| 18 | 40419_at   | -1.62639286532631  | 0   |
| 19 | 37926_at   | -1.59510369191926  | 0   |
| 20 | 40159_r_at | -0.830070056055723 | 0   |

BM - CLL

samples: 8 / 8

*accuracy*

1

*confidence*

1

|   |          |                   |     |
|---|----------|-------------------|-----|
| 1 | 39070_at | 6.29661458968093  | 0 * |
| 2 | 37755_at | 4.71476584328837  | 0 * |
| 3 | 33963_at | 4.63206684324173  | 0   |
| 4 | 38415_at | -4.49254544394577 | 0   |

|    |            |                   |   |
|----|------------|-------------------|---|
| 5  | 36123_at   | 4.12198883271914  | 0 |
| 6  | 37615_at   | 3.82297014835908  | 0 |
| 7  | 38116_at   | 3.70165567234484  | 0 |
| 8  | 38414_at   | 3.60409203763551  | 0 |
| 9  | 41220_at   | -3.59882846329979 | 0 |
| 10 | 34871_at   | -3.59319336097498 | 0 |
| 11 | 35643_at   | 3.56571508955085  | 0 |
| 12 | 1096_g_at  | -3.51858708122275 | 0 |
| 13 | 33386_at   | 3.50471765190995  | 0 |
| 14 | 1884_s_at  | 3.48564292772594  | 0 |
| 15 | 37149_s_at | 3.4769522926405   | 0 |
| 16 | 820_at     | 3.37687376127416  | 0 |
| 17 | 38269_at   | -3.31356010895055 | 0 |
| 18 | 35995_at   | 3.26267624054277  | 0 |
| 19 | 33358_at   | 3.25001188548107  | 0 |
| 20 | 33284_at   | 3.23482135945872  | 0 |

BM - CML

samples: 8 / 10

|    |                   |                   |   |   |
|----|-------------------|-------------------|---|---|
|    | <i>accuracy</i>   | 1                 |   |   |
|    | <i>confidence</i> | 1                 |   |   |
| 1  | 37625_at          | 2.87622426554922  | 0 | * |
| 2  | 41609_at          | 2.52321020501761  | 0 | * |
| 3  | 36661_s_at        | 2.51057654386246  | 0 |   |
| 4  | 1911_s_at         | -2.42145340446397 | 0 |   |
| 5  | 854_at            | 2.37696256335487  | 0 |   |
| 6  | 36773_f_at        | 2.32488494287137  | 0 |   |
| 7  | 35016_at          | 2.24094140253387  | 0 |   |
| 8  | 33274_f_at        | 2.21051775352204  | 0 |   |
| 9  | 38112_g_at        | 2.13305817504128  | 0 |   |
| 10 | 38194_s_at        | 2.09822821859324  | 0 |   |
| 11 | 41165_g_at        | 2.09291822272078  | 0 |   |
| 12 | 33273_f_at        | 2.0687446585274   | 0 |   |
| 13 | 39179_at          | -2.04974106118371 | 0 |   |
| 14 | 432_s_at          | 2.01424464352775  | 0 |   |
| 15 | 36588_at          | 1.99886555057795  | 0 |   |
| 16 | 39968_at          | -1.98085064661371 | 0 |   |

|    |          |                  |   |
|----|----------|------------------|---|
| 17 | 1385_at  | 1.98022588084225 | 0 |
| 18 | 36629_at | -1.9763991250365 | 0 |
| 19 | 38728_at | 1.95859957483225 | 0 |
| 20 | 38472_at | 1.95627106051459 | 0 |

## CLL - CML

samples: 8 / 10

*accuracy*

1

*confidence*

1

|    |            |                   |   |   |
|----|------------|-------------------|---|---|
| 1  | 1105_s_at  | 6.65345823459692  | 0 | * |
| 2  | 41609_at   | 5.09272743129851  | 0 | * |
| 3  | 1096_g_at  | 4.79791769602114  | 0 |   |
| 4  | 34210_at   | 4.5885400157468   | 0 |   |
| 5  | 36155_at   | 4.51821220572632  | 0 |   |
| 6  | 36766_at   | -4.38087516961473 | 0 |   |
| 7  | 41220_at   | 4.30356291392085  | 0 |   |
| 8  | 41165_g_at | 4.29933289075313  | 0 |   |
| 9  | 37625_at   | 4.27214024229386  | 0 |   |
| 10 | 37027_at   | 4.17726581707744  | 0 |   |

|    |            |                   |   |
|----|------------|-------------------|---|
| 11 | 34871_at   | 4.11725674890371  | 0 |
| 12 | 38095_i_at | 4.01294758950756  | 0 |
| 13 | 38578_at   | 3.96024474623017  | 0 |
| 14 | 38116_at   | -3.93637939332745 | 0 |
| 15 | 35643_at   | -3.90694033464584 | 0 |
| 16 | 38833_at   | 3.90073371467641  | 0 |
| 17 | 41164_at   | 3.89237729890143  | 0 |
| 18 | 37344_at   | 3.8687581898534   | 0 |
| 19 | 39670_at   | 3.86448376068684  | 0 |
| 20 | 35016_at   | 3.74007150430317  | 0 |

**2. Analyse: analysis of AML subtypes according to the WHO nomenclature**

**AMLMLL -** samples: 10 / 45

*accuracy* 1

*confidence* 0.92125170098711

|   |          |                  |   |   |
|---|----------|------------------|---|---|
| 1 | 34306_at | 1.36682833853864 | 0 | * |
| 2 | 36881_at | 1.25743716610113 | 0 | * |

|    |            |                   |   |   |
|----|------------|-------------------|---|---|
| 3  | 38994_at   | 1.25633105431216  | 0 | * |
| 4  | 38485_at   | 1.20820491820515  | 0 |   |
| 5  | 32696_at   | 1.20289326580336  | 0 |   |
| 6  | 1983_at    | -1.20116171703008 | 0 |   |
| 7  | 37026_at   | -1.18461413291823 | 0 |   |
| 8  | 138_at     | 1.18310205413783  | 0 |   |
| 9  | 38812_at   | -1.17846157492535 | 0 |   |
| 10 | 33284_at   | -1.16681898560395 | 0 |   |
| 11 | 32232_at   | 1.14845507137154  | 0 |   |
| 12 | 39921_at   | 1.13232410733091  | 0 |   |
| 13 | 34679_at   | -1.12714040987389 | 0 |   |
| 14 | 37992_s_at | 1.11986637618528  | 0 |   |
| 15 | 37029_at   | 1.06646924971963  | 0 |   |
| 16 | 40775_at   | -1.06615341562387 | 0 |   |
| 17 | 36709_at   | 1.04614233632581  | 0 |   |
| 18 | 37809_at   | 1.03749230715704  | 0 |   |
| 19 | 38097_at   | 1.03525254247508  | 0 |   |
| 20 | 36608_at   | 0.747544727295107 | 0 |   |

| AMLMLL - INV16    |            | samples: 10 / 10  |     |
|-------------------|------------|-------------------|-----|
| <i>accuracy</i>   |            | 1                 |     |
| <i>confidence</i> |            | 1                 |     |
| 1                 | 38812_at   | -3.34686451971904 | 0 * |
| 2                 | 37407_s_at | -3.22294767554078 | 0   |
| 3                 | 35282_r_at | 2.34298696520172  | 0 * |
| 4                 | 37026_at   | -2.25660818336648 | 0   |
| 5                 | 33856_at   | 2.25212063750729  | 0   |
| 6                 | 32174_at   | -2.16867472363265 | 0   |
| 7                 | 33284_at   | -2.14901777919516 | 0   |
| 8                 | 38653_at   | -2.09296931036988 | 0   |
| 9                 | 1983_at    | -2.06674088426528 | 0   |
| 10                | 32696_at   | 2.03331671439074  | 0   |
| 11                | 767_at     | -1.99007511677258 | 0   |
| 12                | 35329_at   | 1.92663715318122  | 0   |
| 13                | 36881_at   | 1.88821561232545  | 0   |
| 14                | 40767_at   | -1.84600140068058 | 0   |



|    |          |                   |   |
|----|----------|-------------------|---|
| 15 | 36095_at | -1.77023425026019 | 0 |
| 16 | 538_at   | -1.75720288873792 | 0 |
| 17 | 33319_at | 1.6982626829354   | 0 |
| 18 | 38485_at | 1.69464482881744  | 0 |
| 19 | 38747_at | -1.69240449076905 | 0 |
| 20 | 38994_at | 1.50803351291881  | 0 |

# AMLMLL - OTHER

samples: 10 / 10

*accuracy*

1

*confidence*

0.972144217378764

|   |          |                   |   |   |
|---|----------|-------------------|---|---|
| 1 | 36980_at | -1.34035598763443 | 0 | * |
| 2 | 100_g_at | 1.32781895440119  | 0 | * |
| 3 | 38994_at | 1.27848227020726  | 0 |   |
| 4 | 37029_at | 1.27656800999718  | 0 |   |
| 5 | 37026_at | -1.24955259337174 | 0 | * |
| 6 | 37417_at | 1.19110502379759  | 0 | * |
| 7 | 39993_at | -1.18099046398082 | 0 |   |
| 8 | 39118_at | -1.1584453284446  | 0 |   |

|    |            |                   |   |
|----|------------|-------------------|---|
| 9  | 36881_at   | 1.12737149627183  | 0 |
| 10 | 34251_at   | -1.12590878042921 | 0 |
| 11 | 35813_at   | 1.10960381779872  | 0 |
| 12 | 138_at     | 1.09814796011793  | 0 |
| 13 | 36945_at   | 1.09593061163621  | 0 |
| 14 | 40281_at   | 1.083400522626    | 0 |
| 15 | 35941_f_at | 1.0833686449051   | 0 |
| 16 | 36952_at   | 1.069544205786    | 0 |
| 17 | 37403_at   | -1.06943971961994 | 0 |
| 18 | 33689_s_at | 1.06337639894231  | 0 |
| 19 | 35372_r_at | -1.05302441823616 | 0 |
| 20 | 32072_at   | 1.02664886940357  | 0 |

AMLMLL - T1517

samples: 10 / 16

*accuracy*

1

*confidence*

1

|   |          |                  |   |   |
|---|----------|------------------|---|---|
| 1 | 39649_at | 3.23957503042803 | 0 | * |
| 2 | 38435_at | 2.60733219271303 | 0 | * |

|    |            |                   |   |
|----|------------|-------------------|---|
| 3  | 38097_at   | 2.52025252941371  | 0 |
| 4  | 32229_at   | 2.40682119042641  | 0 |
| 5  | 38487_at   | -2.31348932548076 | 0 |
| 6  | 32696_at   | 2.21878031159682  | 0 |
| 7  | 38485_at   | 2.10692284528305  | 0 |
| 8  | 33284_at   | -2.09299435714406 | 0 |
| 9  | 38824_at   | 2.08124417022995  | 0 |
| 10 | 41138_at   | -2.03312026813146 | 0 |
| 11 | 37967_at   | 1.92254422115649  | 0 |
| 12 | 33866_at   | -1.91543446589406 | 0 |
| 13 | 32543_at   | -1.87715920226866 | 0 |
| 14 | 1983_at    | -1.87444715294745 | 0 |
| 15 | 35823_at   | -1.86189545486519 | 0 |
| 16 | 36749_at   | -1.81025193870165 | 0 |
| 17 | 38063_at   | -1.7878938995328  | 0 |
| 18 | 39814_s_at | -1.75490742013487 | 0 |
| 19 | 36843_at   | 1.74046122003025  | 0 |
| 20 | 38992_at   | 1.71753799928796  | 0 |

| AMLMLL - T821 |                   | samples: 10 / 9   |   |   |
|---------------|-------------------|-------------------|---|---|
|               | <i>accuracy</i>   | 1                 |   |   |
|               | <i>confidence</i> | 1                 |   |   |
| 1             | 36881_at          | 2.29294544811647  | 0 | * |
| 2             | 32323_at          | -1.98347658852059 | 0 | * |
| 3             | 37811_at          | -1.98247325351143 | 0 |   |
| 4             | 38391_at          | 1.94083259845207  | 0 |   |
| 5             | 33412_at          | 1.92827460657744  | 0 |   |
| 6             | 33284_at          | -1.8385557317965  | 0 |   |
| 7             | 33856_at          | 1.77909423724864  | 0 |   |
| 8             | 38097_at          | 1.75444250975416  | 0 |   |
| 9             | 34679_at          | -1.72476579402037 | 0 |   |
| 10            | 37399_at          | -1.70947276971912 | 0 |   |
| 11            | 36571_at          | 1.65482279043264  | 0 |   |
| 12            | 35638_at          | -1.65089605723885 | 0 |   |
| 13            | 32696_at          | 1.63638794888669  | 0 |   |
| 14            | 32184_at          | 1.62897781786406  | 0 |   |

|    |           |                   |   |
|----|-----------|-------------------|---|
| 15 | 1911_s_at | -1.61083786198679 | 0 |
| 16 | 34306_at  | 1.59626133274337  | 0 |
| 17 | 138_at    | 1.59241136884495  | 0 |
| 18 | 41694_at  | -1.55909099909815 | 0 |
| 19 | 32232_at  | 1.54494819348846  | 0 |
| 20 | 36608_at  | 1.1358211663482   | 0 |

## INV16 -

samples: 10 / 45

*accuracy*

1

*confidence*

1

|   |            |                   |   |   |
|---|------------|-------------------|---|---|
| 1 | 37407_s_at | 3.02509409963287  | 0 | * |
| 2 | 767_at     | 1.85632628490303  | 0 | * |
| 3 | 245_at     | 1.70794453836984  | 0 |   |
| 4 | 35282_r_at | -1.55233894025198 | 0 |   |
| 5 | 38465_at   | 1.52686366669143  | 0 |   |
| 6 | 36095_at   | 1.40576248502182  | 0 |   |
| 7 | 32174_at   | 1.39467340729953  | 0 |   |
| 8 | 1385_at    | 1.35491176363704  | 0 |   |

|    |           |                   |   |
|----|-----------|-------------------|---|
| 9  | 41609_at  | 1.33680396130546  | 0 |
| 10 | 36607_at  | 1.31728883029627  | 0 |
| 11 | 34210_at  | 1.25533053163606  | 0 |
| 12 | 33731_at  | 1.18379724417068  | 0 |
| 13 | 2019_s_at | 1.1724338503802   | 0 |
| 14 | 40456_at  | -1.17211851173852 | 0 |
| 15 | 277_at    | 1.16888798816433  | 0 |
| 16 | 931_at    | 1.16565119574672  | 0 |
| 17 | 37762_at  | 1.14260401763247  | 0 |
| 18 | 35230_at  | 1.13832458283537  | 0 |
| 19 | 34780_at  | 1.12142169279465  | 0 |
| 20 | 41200_at  | 1.10294533672324  | 0 |

## INV16 - OTHER

samples: 10 / 10

accuracy 1

confidence 1

|   |            |                  |   |   |
|---|------------|------------------|---|---|
| 1 | 37407_s_at | 3.18736190788495 | 0 | * |
| 2 | 37600_at   | 2.62690062253569 | 0 | * |

|    |            |                  |   |
|----|------------|------------------|---|
| 3  | 767_at     | 2.03572561609575 | 0 |
| 4  | 41609_at   | 1.96219869102861 | 0 |
| 5  | 32174_at   | 1.91764639873215 | 0 |
| 6  | 41723_s_at | 1.8341348306376  | 0 |
| 7  | 38833_at   | 1.8197922525705  | 0 |
| 8  | 38465_at   | 1.80863491318623 | 0 |
| 9  | 38095_i_at | 1.80209304301982 | 0 |
| 10 | 1230_g_at  | 1.64339686952341 | 0 |
| 11 | 1252_at    | 1.59751061992943 | 0 |
| 12 | 32434_at   | -1.5885630305188 | 0 |
| 13 | 40856_at   | 1.50737403239702 | 0 |
| 14 | 37762_at   | 1.49715599199852 | 0 |
| 15 | 37344_at   | 1.46932515754743 | 0 |
| 16 | 35016_at   | 1.44723563131209 | 0 |
| 17 | 35078_at   | 1.44013020473382 | 0 |
| 18 | 37001_at   | 1.43580114615375 | 0 |
| 19 | 33920_at   | 1.39389220008214 | 0 |
| 20 | 245_at     | 1.37591797605968 | 0 |

## INV16 - T1517

samples: 10 / 16

*accuracy*

1

*confidence*

1

|    |            |                  |   |   |
|----|------------|------------------|---|---|
| 1  | 245_at     | 4.57658935261639 | 0 | * |
| 2  | 38833_at   | 4.25223366871621 | 0 | * |
| 3  | 38095_i_at | 3.57578878481709 | 0 |   |
| 4  | 39649_at   | 3.23025693895729 | 0 |   |
| 5  | 38096_f_at | 3.14225313100266 | 0 |   |
| 6  | 35016_at   | 3.0787769409051  | 0 |   |
| 7  | 38435_at   | 3.03350943051849 | 0 |   |
| 8  | 37039_at   | 2.97439961013438 | 0 |   |
| 9  | 38465_at   | 2.96526060073085 | 0 |   |
| 10 | 37407_s_at | 2.87881711895892 | 0 |   |
| 11 | 34210_at   | 2.84796613729927 | 0 |   |
| 12 | 41723_s_at | 2.82100515486823 | 0 |   |
| 13 | 41471_at   | 2.80737102015788 | 0 |   |
| 14 | 34789_at   | 2.75455608102168 | 0 |   |



|    |           |                  |   |
|----|-----------|------------------|---|
| 15 | 1052_s_at | 2.6975735697327  | 0 |
| 16 | 36601_at  | 2.67187833778929 | 0 |
| 17 | 41096_at  | 2.59449996104956 | 0 |
| 18 | 41609_at  | 2.57402348086536 | 0 |
| 19 | 37344_at  | 2.56147220347162 | 0 |
| 20 | 40698_at  | 2.54689030859799 | 0 |

## INV16 - T821

samples: 10 / 9

*accuracy*

1

*confidence*

1

|   |            |                  |   |   |
|---|------------|------------------|---|---|
| 1 | 37407_s_at | 3.01984756968935 | 0 | * |
| 2 | 2019_s_at  | 2.27319677276044 | 0 |   |
| 3 | 36607_at   | 2.26121735205867 | 0 |   |
| 4 | 41535_at   | 2.20248916475367 | 0 | * |
| 5 | 40198_at   | 1.86811562002606 | 0 |   |
| 6 | 35264_at   | 1.84583120098715 | 0 |   |
| 7 | 36661_s_at | 1.8131267115673  | 0 |   |
| 8 | 36095_at   | 1.79878279442616 | 0 |   |

|    |          |                   |   |
|----|----------|-------------------|---|
| 9  | 32747_at | 1.78653441127702  | 0 |
| 10 | 40718_at | 1.77233756136773  | 0 |
| 11 | 37326_at | 1.76038682206377  | 0 |
| 12 | 34780_at | 1.74785276488982  | 0 |
| 13 | 39610_at | 1.74122046729845  | 0 |
| 14 | 33390_at | 1.73740374189728  | 0 |
| 15 | 767_at   | 1.72097134093781  | 0 |
| 16 | 32080_at | -1.70225469167763 | 0 |
| 17 | 39358_at | 1.695944330956    | 0 |
| 18 | 37747_at | 1.67498682162383  | 0 |
| 19 | 245_at   | 1.65171897393137  | 0 |
| 20 | 33731_at | 1.62582771838167  | 0 |

**OTHER -**

samples: 10 / 45

*accuracy*

0.981818181818182

*confidence*

0.981818181818182

|   |          |                  |   |   |
|---|----------|------------------|---|---|
| 1 | 34251_at | 1.12590878042921 | 0 | * |
| 2 | 37018_at | 1.10268143578403 | 0 |   |

|    |            |                         |
|----|------------|-------------------------|
| 3  | 33920_at   | -0.956076703831482 0    |
| 4  | 35941_f_at | -0.90383440767488 0     |
| 5  | 256_s_at   | -0.858111816204111 0.01 |
| 6  | 37333_at   | 0.8275447098375 0       |
| 7  | 32434_at   | 0.805850409739795 0     |
| 8  | 1959_at    | 0.796925434525945 0     |
| 9  | 37147_at   | -0.773953141034502 0    |
| 10 | 33284_at   | -0.771438360960095 0    |
| 11 | 40864_at   | -0.770641950715737 0    |
| 12 | 35154_at   | -0.764874807980337 0    |
| 13 | 2047_s_at  | -0.748787188622726 0    |
| 14 | 41763_g_at | 0.748545954599463 0     |
| 15 | 36900_at   | -0.74265889729539 0     |
| 16 | 33351_at   | 0.742532920653334 0     |
| 17 | 36936_at   | 0.733922207115175 0     |
| 18 | 37263_at   | 0.729044492680672 0     |
| 19 | 38695_at   | -0.71970619250199 0     |
| 20 | 40509_at   | 0.712799214281053 0     |

## OTHER - T1517

samples: 10 / 16

*accuracy*

1

*confidence*

1

|    |            |                   |   |   |
|----|------------|-------------------|---|---|
| 1  | 39649_at   | 3.30712305398492  | 0 | * |
| 2  | 40718_at   | -2.52673625599382 | 0 | * |
| 3  | 39775_at   | -1.97869028082043 | 0 |   |
| 4  | 34789_at   | 1.95413968158198  | 0 |   |
| 5  | 32543_at   | -1.91464724323262 | 0 |   |
| 6  | 34110_g_at | -1.77793772892734 | 0 |   |
| 7  | 38487_at   | -1.76846306892822 | 0 |   |
| 8  | 40493_at   | -1.6739728895294  | 0 |   |
| 9  | 40698_at   | 1.65346991374979  | 0 |   |
| 10 | 41273_at   | -1.61494643368443 | 0 |   |
| 11 | 33284_at   | -1.59460520214407 | 0 |   |
| 12 | 32434_at   | 1.57854380538056  | 0 |   |
| 13 | 39755_at   | -1.57527382190822 | 0 |   |
| 14 | 40817_at   | -1.54437681308404 | 0 |   |

|    |          |                   |   |
|----|----------|-------------------|---|
| 15 | 37408_at | -1.53683716438534 | 0 |
| 16 | 33102_at | 1.53530070976794  | 0 |
| 17 | 1752_at  | -1.52886252404363 | 0 |
| 18 | 37954_at | -1.5109989255419  | 0 |
| 19 | 38791_at | -1.48386160940786 | 0 |
| 20 | 34210_at | 1.44938674947878  | 0 |

**OTHER - T821**

samples: 10 / 9

*accuracy*

1

*confidence*

0.994837795579117

|   |            |                   |   |   |
|---|------------|-------------------|---|---|
| 1 | 32323_at   | -1.94417836607133 | 0 | * |
| 2 | 37811_at   | -1.61775423684388 | 0 | * |
| 3 | 34512_at   | -1.39224768490919 | 0 |   |
| 4 | 37809_at   | 1.31872220085798  | 0 |   |
| 5 | 40585_at   | 1.31087716877391  | 0 |   |
| 6 | 33284_at   | -1.29020750912798 | 0 |   |
| 7 | 38096_f_at | -1.25756828218199 | 0 |   |
| 8 | 36973_at   | 1.23300907353238  | 0 |   |

|    |                         |                   |   |
|----|-------------------------|-------------------|---|
| 9  | 35940_at                | -1.20559489876876 | 0 |
| 10 | 38808_at                | -1.18153953430958 | 0 |
| 11 | 37333_at                | 1.17979557242332  | 0 |
| 12 | 2047_s_at               | -1.17934561734238 | 0 |
| 13 | AFFX-HUMRGE/M10098_M_at | -1.15756874447998 | 0 |
| 14 | 958_s_at                | 1.1376378956      | 0 |
| 15 | 34251_at                | 1.12590878042921  | 0 |
| 16 | 38963_i_at              | -1.12200244261352 | 0 |
| 17 | 35638_at                | -1.12014975713644 | 0 |
| 18 | 38095_i_at              | -1.10572791785236 | 0 |
| 19 | 37657_at                | -1.08109523793911 | 0 |
| 20 | 40718_at                | 0.918288266614732 | 0 |

T1517 - samples: 16 / 39

*accuracy* 1

*confidence* 0.99537936517205

|   |          |                   |   |   |
|---|----------|-------------------|---|---|
| 1 | 39649_at | -3.29831494694965 | 0 | * |
| 2 | 40718_at | 2.08511115510612  | 0 | * |

|    |            |                   |   |   |
|----|------------|-------------------|---|---|
| 3  | 38487_at   | 2.00096141225403  | 0 | * |
| 4  | 34110_g_at | 1.76946763277471  | 0 |   |
| 5  | 34789_at   | -1.70643590139573 | 0 |   |
| 6  | 38435_at   | -1.66171359352607 | 0 |   |
| 7  | 32543_at   | 1.59263172662039  | 0 |   |
| 8  | 41273_at   | 1.54397178886438  | 0 |   |
| 9  | 40493_at   | 1.48615605789895  | 0 |   |
| 10 | 38096_f_at | -1.44819099507958 | 0 |   |
| 11 | 41471_at   | -1.41828217671556 | 0 |   |
| 12 | 37954_at   | 1.41406051783378  | 0 |   |
| 13 | 33454_at   | 1.39832642238269  | 0 |   |
| 14 | 38791_at   | 1.38083401177366  | 0 |   |
| 15 | 41096_at   | -1.36447605743032 | 0 |   |
| 16 | 1752_at    | 1.36363148385769  | 0 |   |
| 17 | 38833_at   | -1.34891815086687 | 0 |   |
| 18 | 210_at     | -1.34320613976446 | 0 |   |
| 19 | 35016_at   | -1.33685666840696 | 0 |   |
| 20 | 37669_s_at | 0.806171390298286 | 0 |   |

| T1517 - T821      |            | samples: 16 / 9   |   |   |
|-------------------|------------|-------------------|---|---|
| <i>accuracy</i>   |            | 1                 |   |   |
| <i>confidence</i> |            | 1                 |   |   |
| 1                 | 40718_at   | 3.23930438679201  | 0 | * |
| 2                 | 39649_at   | -3.19787649222746 | 0 | * |
| 3                 | 40698_at   | -3.08468795621776 | 0 |   |
| 4                 | 38096_f_at | -2.65789275034265 | 0 |   |
| 5                 | 39775_at   | 2.36672318019601  | 0 |   |
| 6                 | 38487_at   | 2.29609697942891  | 0 |   |
| 7                 | 33121_g_at | -2.21859945215003 | 0 |   |
| 8                 | 35016_at   | -1.96619441751917 | 0 |   |
| 9                 | 38095_i_at | -1.91141006266887 | 0 |   |
| 10                | 32506_at   | -1.88419268611225 | 0 |   |
| 11                | 38833_at   | -1.85079137548356 | 0 |   |
| 12                | 34110_g_at | 1.85075648886345  | 0 |   |
| 13                | 41096_at   | -1.8279606340398  | 0 |   |
| 14                | 38391_at   | 1.81966548635468  | 0 |   |



|    |          |                   |   |
|----|----------|-------------------|---|
| 15 | 35766_at | 1.75448820173577  | 0 |
| 16 | 34789_at | -1.71046499814806 | 0 |
| 17 | 41609_at | -1.710217028597   | 0 |
| 18 | 41273_at | 1.70663861548637  | 0 |
| 19 | 37344_at | -1.69281730857466 | 0 |
| 20 | 35340_at | 1.69006593600413  | 0 |

T821 -

samples: 9 / 46

*accuracy*

1

*confidence*

0.920027437519393

|   |          |                   |   |   |
|---|----------|-------------------|---|---|
| 1 | 37811_at | 1.59605072597366  | 0 | * |
| 2 | 38391_at | -1.3878317468135  | 0 |   |
| 3 | 35638_at | 1.38266687057184  | 0 | * |
| 4 | 32323_at | 1.35561326937612  | 0 |   |
| 5 | 35940_at | 1.20094762805468  | 0 | * |
| 6 | 36973_at | -1.17706120019907 | 0 |   |
| 7 | 35264_at | -1.10943417036523 | 0 |   |
| 8 | 361_at   | 1.07264489085601  | 0 |   |

|    |            |                    |     |
|----|------------|--------------------|-----|
| 9  | 36802_at   | -1.02457173409803  | 0   |
| 10 | 34512_at   | 1.0204248889286    | 0   |
| 11 | 35939_s_at | 0.955125481450532  | 0   |
| 12 | 39061_at   | -0.947115729172708 | 0   |
| 13 | 37326_at   | -0.935233446940231 | 0   |
| 14 | 32747_at   | -0.930843404980031 | 0   |
| 15 | 1096_g_at  | 0.927398573506987  | 0   |
| 16 | 33121_g_at | 0.923255276498333  | 0 * |
| 17 | 41535_at   | -0.916652918883009 | 0   |
| 18 | 37023_at   | -0.915934376270622 | 0   |
| 19 | 38780_at   | -0.915816135921152 | 0   |

### 3. Analyse: analysis of ALL subtypes

|            |          |                  |        |
|------------|----------|------------------|--------|
| ALL814 -   |          | samples: 3 / 14  |        |
| accuracy   |          | 1                |        |
| confidence |          | 1                |        |
| 1          | 1402_at  | 2.08175003568258 | 0.01 * |
| 2          | 37747_at | 2.03525291878921 | 0 *    |

|    |           |                   |      |
|----|-----------|-------------------|------|
| 3  | 37701_at  | 1.72252048284758  | 0.01 |
| 4  | 2042_s_at | -1.63373519277864 | 0    |
| 5  | 35260_at  | -1.63074548017429 | 0    |
| 6  | 1476_s_at | -1.58695680100552 | 0    |
| 7  | 32616_at  | 1.57366205688451  | 0    |
| 8  | 932_i_at  | -1.57233356229385 | 0    |
| 9  | 36139_at  | -1.5665197341194  | 0    |
| 10 | 39730_at  | -1.5464188647031  | 0.01 |
| 11 | 2024_s_at | 1.48918618192137  | 0.01 |
| 12 | 38730_at  | -1.45475301578891 | 0.01 |
| 13 | 37021_at  | 1.45440716568168  | 0    |
| 14 | 933_f_at  | -1.42175300666003 | 0    |
| 15 | 41396_at  | -1.38553827410353 | 0    |
| 16 | 33856_at  | 1.37781449850137  | 0    |
| 17 | 33905_at  | 1.3359321134002   | 0.01 |

ALL814 - ALLMLL

samples: 3 / 4

accuracy

1

|    | <i>confidence</i> | 1                      |   |
|----|-------------------|------------------------|---|
| 1  | 2042_s_at         | -8.02342094912714 0.05 | * |
| 2  | 36638_at          | -4.58127332202829 0.02 |   |
| 3  | 1474_s_at         | -4.09073883260025 0.03 | * |
| 4  | 706_at            | -3.85465872728703 0.02 |   |
| 5  | 38994_at          | -3.74888987537358 0.02 |   |
| 6  | 34785_at          | -3.3713121522884 0.03  |   |
| 7  | 36798_g_at        | -3.35179120581516 0    |   |
| 8  | 41191_at          | -3.25108066126486 0.01 |   |
| 9  | 39827_at          | -3.14944671750591 0.02 |   |
| 10 | 585_at            | -3.09495658747361 0.04 |   |
| 11 | 2069_s_at         | -3.01980201927276 0.02 |   |
| 12 | 529_at            | 2.93352551602605 0.01  |   |
| 13 | 307_at            | 2.92372091093276 0.03  |   |
| 14 | 32842_at          | -2.85788132874268 0.01 |   |
| 15 | 36873_at          | -2.84199424616029 0.05 |   |
| 16 | 41747_s_at        | -2.76420890085279 0.01 |   |

| ALL814 - ALLPH |                   | samples: 3 / 7    |        |
|----------------|-------------------|-------------------|--------|
|                | <i>accuracy</i>   | 1                 |        |
|                | <i>confidence</i> | 1                 |        |
| 1              | 35260_at          | -2.82900147590099 | 0.01 * |
| 2              | 41177_at          | 2.74938757132087  | 0 *    |
| 3              | 36638_at          | -2.41641563333395 | 0.01   |
| 4              | 38767_at          | -2.40416010568405 | 0.01   |
| 5              | 37747_at          | 2.39180707441687  | 0      |
| 6              | 39327_at          | -2.27856651600595 | 0      |
| 7              | 1476_s_at         | -2.09613072968554 | 0.02   |
| 8              | 1636_g_at         | -2.00644064085741 | 0.01   |
| 9              | 37159_at          | -1.98769010758559 | 0      |
| 10             | 932_i_at          | -1.95869341917388 | 0      |
| 11             | 38994_at          | -1.94783634512686 | 0.02   |
| 12             | 1402_at           | 1.91294884399227  | 0      |
| 13             | 32319_at          | -1.89265256004687 | 0.01   |
| 14             | 2047_s_at         | -1.89118154910995 | 0      |
| 15             | 40936_at          | -1.84560154590494 | 0      |

|    |          |                   |      |
|----|----------|-------------------|------|
| 16 | 39730_at | -1.84157870686046 | 0.03 |
| 17 | 39089_at | -1.83344549691856 | 0    |
| 18 | 41734_at | -1.82721322918029 | 0.01 |
| 19 | 39755_at | -1.80690655801942 | 0.03 |

**ALL814 - ALLT**

samples: 3 / 3

*accuracy*

1

*confidence*

1

|   |          |                   |      |   |
|---|----------|-------------------|------|---|
| 1 | 36103_at | 3.43807291883285  | 0.01 | * |
| 2 | 35350_at | 3.3144051465682   | 0.04 |   |
| 3 | 41654_at | -3.10101195313041 | 0.04 | * |

**ALLMLL -**

samples: 4 / 13

*accuracy*

1

*confidence*

1

|   |          |                  |   |   |
|---|----------|------------------|---|---|
| 1 | 36873_at | 2.83046978285357 | 0 | * |
| 2 | 36638_at | 2.81082924166381 | 0 | * |
| 3 | 33358_at | 2.41284542345819 | 0 |   |

|    |            |                  |      |
|----|------------|------------------|------|
| 4  | 34785_at   | 2.01800062696643 | 0    |
| 5  | 36667_at   | 2.00264026114972 | 0    |
| 6  | 41503_at   | 1.98278140811591 | 0    |
| 7  | 36690_at   | 1.97928285044649 | 0.01 |
| 8  | 706_at     | 1.96737076450007 | 0    |
| 9  | 32842_at   | 1.88883935305863 | 0    |
| 10 | 41747_s_at | 1.87619134543011 | 0    |
| 11 | 32145_at   | 1.87136682311337 | 0    |
| 12 | 36798_g_at | 1.76515008934463 | 0.01 |
| 13 | 41191_at   | 1.7369773616741  | 0    |
| 14 | 40763_at   | 1.69441997605083 | 0    |
| 15 | 585_at     | 1.66246850330104 | 0    |
| 16 | 41470_at   | 1.53671027688439 | 0    |
| 17 | 40786_at   | 1.52293758990032 | 0    |
| 18 | 38037_at   | 1.50762328192198 | 0.01 |
| 19 | 34583_at   | 1.46227478562542 | 0    |
| 20 | 1140_at    | 1.46133065433595 | 0    |

| ALLMLL - ALLPH |                   | samples: 4 / 7    |      |   |
|----------------|-------------------|-------------------|------|---|
|                | <i>accuracy</i>   | 1                 |      |   |
|                | <i>confidence</i> | 1                 |      |   |
| 1              | 40723_at          | 3.55841873411154  | 0    | * |
| 2              | 706_at            | 3.32668949661753  | 0    | * |
| 3              | 41191_at          | 2.96542484991746  | 0    |   |
| 4              | 36638_at          | 2.84067512400178  | 0    |   |
| 5              | 36873_at          | 2.8258041781711   | 0    |   |
| 6              | 36690_at          | 2.54358082956883  | 0    |   |
| 7              | 33358_at          | 2.34079500414888  | 0    |   |
| 8              | 36798_g_at        | 2.21311555975342  | 0.01 |   |
| 9              | 36667_at          | 2.20932580996057  | 0.01 |   |
| 10             | 41177_at          | 2.1413450003396   | 0    |   |
| 11             | 40865_at          | 2.11221046250059  | 0    |   |
| 12             | 37967_at          | -2.08412772392346 | 0    |   |
| 13             | 34892_at          | -2.08369333371306 | 0    |   |
| 14             | 40396_at          | 1.96552338894503  | 0    |   |
| 15             | 1140_at           | 1.96261636340905  | 0    |   |



|    |          |                   |      |
|----|----------|-------------------|------|
| 16 | 33134_at | -1.95145751139773 | 0    |
| 17 | 32842_at | 1.84503319654406  | 0    |
| 18 | 41503_at | 1.8284794750916   | 0    |
| 19 | 32145_at | 1.82248695271075  | 0    |
| 20 | 40763_at | 1.78804175908387  | 0.01 |

## ALLMLL - ALLT

samples: 4 / 3

*accuracy*

1

*confidence*

1

|   |            |                   |      |   |
|---|------------|-------------------|------|---|
| 1 | 2069_s_at  | 13.292701923441   | 0    | * |
| 2 | 41153_f_at | 10.2582391724747  | 0    | * |
| 3 | 41156_g_at | 5.75960819662385  | 0.01 |   |
| 4 | 33352_at   | 4.58870845894255  | 0    |   |
| 5 | 36638_at   | 4.58127332202829  | 0.03 |   |
| 6 | 1185_at    | 4.45457229345442  | 0.01 |   |
| 7 | 37775_at   | -4.11123301947466 | 0.02 |   |
| 8 | 1105_s_at  | -4.04867441577307 | 0.03 |   |
| 9 | 41155_at   | 3.98831214950398  | 0.01 |   |

|    |            |                   |      |
|----|------------|-------------------|------|
| 10 | 38994_at   | 3.88924207710779  | 0.02 |
| 11 | 34785_at   | 3.83690018368942  | 0.01 |
| 12 | 32819_at   | 3.567056723698    | 0.03 |
| 13 | 38319_at   | -3.55471475398643 | 0.01 |
| 14 | 2045_s_at  | 3.54943843148795  | 0.02 |
| 15 | 40159_r_at | 3.40746200289675  | 0.03 |
| 16 | 39136_at   | -3.36701895470486 | 0.02 |
| 17 | 1110_at    | -3.33969464270628 | 0.01 |
| 18 | 38017_at   | 3.32515685260135  | 0.01 |
| 19 | 605_at     | -3.28310118648462 | 0.02 |

#### 4. Analyse: other analyses

ALLPH - samples: 7 / 10

accuracy 1

confidence 1

|   |          |                  |   |   |
|---|----------|------------------|---|---|
| 1 | 1389_at  | 1.58617196971584 | 0 | * |
| 2 | 41734_at | 1.55949651759221 | 0 | * |
| 3 | 38336_at | 1.52692526781459 | 0 |   |

|    |            |                   |      |
|----|------------|-------------------|------|
| 4  | 33134_at   | 1.449713769608    | 0    |
| 5  | 36878_f_at | 1.36077477960263  | 0    |
| 6  | 39755_at   | 1.27483851783738  | 0    |
| 7  | 38833_at   | 1.2244093710462   | 0    |
| 8  | 33924_at   | 1.22263315100349  | 0    |
| 9  | 34362_at   | 1.1962046547055   | 0    |
| 10 | 36536_at   | 1.19336569573264  | 0    |
| 11 | 37344_at   | 1.18918159634593  | 0    |
| 12 | 38095_i_at | 1.16331309702494  | 0    |
| 13 | 35260_at   | 1.12932649576543  | 0    |
| 14 | 41177_at   | -1.07976913600882 | 0    |
| 15 | 38096_f_at | 1.05014739949744  | 0.01 |
| 16 | 36773_f_at | 1.0492226005037   | 0    |
| 17 | 39824_at   | 1.03626825828771  | 0    |
| 18 | 31898_at   | 1.02765158070601  | 0    |
| 19 | 1636_g_at  | 1.0227576964995   | 0    |
| 20 | 41609_at   | 0.997013086295946 | 0    |

## ALLPH - ALLT

samples: 7 / 3

|    |                   |                   |      |   |
|----|-------------------|-------------------|------|---|
|    | <i>accuracy</i>   | 1                 |      |   |
|    | <i>confidence</i> | 1                 |      |   |
| 1  | 1105_s_at         | -4.05162267253209 | 0    | * |
| 2  | 38319_at          | -3.66580320533053 | 0.03 | * |
| 3  | 38096_f_at        | 2.88234070062166  | 0.02 |   |
| 4  | 37039_at          | 2.80755189593111  | 0    |   |
| 5  | 35016_at          | 2.77774834690928  | 0.01 |   |
| 6  | 38833_at          | 2.75560710134977  | 0.01 |   |
| 7  | 39262_at          | -2.59234132448068 | 0    |   |
| 8  | 32649_at          | -2.55542908459441 | 0    |   |
| 9  | 33821_at          | -2.5421725262322  | 0.01 |   |
| 10 | 41609_at          | 2.5109183575568   | 0    |   |
| 11 | 38147_at          | -2.50135496035854 | 0    |   |
| 12 | 38095_i_at        | 2.48939716688646  | 0.02 |   |
| 13 | 37739_at          | -2.44732228148107 | 0    |   |
| 14 | 38894_g_at        | 2.42422840620003  | 0.01 |   |
| 15 | 36638_at          | 2.41641563333395  | 0    |   |

|    |            |                   |      |
|----|------------|-------------------|------|
| 16 | 38361_g_at | 2.38116082851993  | 0.01 |
| 17 | 2059_s_at  | -2.37547551809124 | 0.01 |
| 18 | 33425_at   | -2.36441631934975 | 0    |
| 19 | 38949_at   | -2.27455845085004 | 0    |
| 20 | 39755_at   | 2.26518913381284  | 0    |

ALLT -

samples: 3 / 14

*accuracy*

1

*confidence*

1

|   |           |                  |   |   |
|---|-----------|------------------|---|---|
| 1 | 38319_at  | 3.50494628126444 | 0 | * |
| 2 | 33821_at  | 2.86458211053638 | 0 | * |
| 3 | 1105_s_at | 2.7919896009269  | 0 |   |
| 4 | 38147_at  | 2.2999876938771  | 0 |   |
| 5 | 38949_at  | 2.275851563485   | 0 |   |
| 6 | 33425_at  | 2.24691287113975 | 0 |   |
| 7 | 40407_at  | 2.23626457040595 | 0 |   |
| 8 | 1110_at   | 2.23213485898084 | 0 |   |
| 9 | 39136_at  | 2.21536950680885 | 0 |   |

|    |            |                   |      |
|----|------------|-------------------|------|
| 10 | 41535_at   | 2.20104335983474  | 0    |
| 11 | 2059_s_at  | 2.17544015063967  | 0    |
| 12 | 39262_at   | 2.14503507257872  | 0    |
| 13 | 34367_at   | 2.14251924457163  | 0    |
| 14 | 35016_at   | -2.12822205034103 | 0    |
| 15 | 38096_f_at | -2.0151362322022  | 0    |
| 16 | 37775_at   | 2.0098435918241   | 0.01 |
| 17 | 38917_at   | 2.00844440766432  | 0    |
| 18 | 33238_at   | 2.00529430466423  | 0    |
| 19 | 1498_at    | 1.98727437856937  | 0    |
| 20 | 41163_at   | 1.90540704553591  | 0    |

ALLPHNEG - ALLPHPOS

samples: 11 / 7

*accuracy*

1

*confidence*

0.946908445764721

|   |          |                   |   |   |
|---|----------|-------------------|---|---|
| 1 | 38336_at | -1.5382379030083  | 0 | * |
| 2 | 33134_at | -1.30650437502273 | 0 | * |
| 3 | 39755_at | -1.28612797222091 | 0 |   |

|    |            |                      |
|----|------------|----------------------|
| 4  | 1636_g_at  | -1.04852861613762 0  |
| 5  | 38833_at   | -1.04767357167583 0  |
| 6  | 41177_at   | 1.04154428480732 0   |
| 7  | 34168_at   | -1.00022056220148 0  |
| 8  | 38096_f_at | -0.991139993364388 0 |
| 9  | 38095_i_at | -0.969632957696579 0 |
| 10 | 33924_at   | -0.965257886268051 0 |
| 11 | 39756_g_at | -0.964856826724863 0 |
| 12 | 38312_at   | -0.964240310753493 0 |
| 13 | 36878_f_at | -0.961827994429321 0 |
| 14 | 41193_at   | -0.957818027300299 0 |
| 15 | 37384_at   | -0.934644823332001 0 |
| 16 | 32706_at   | 0.916645445316056 0  |
| 17 | 33441_at   | -0.910220742840358 0 |
| 18 | 41547_at   | 0.895837845645142 0  |
| 19 | 36773_f_at | -0.884139970624711 0 |
| 20 | 32649_at   | 0.833759113455451 0  |

Table 21

| Affy<br>met<br>rix_<br>ID | Description_microarray  | Symbo<br>l  | Description_Net<br>Affx                                 | Chrom<br>osome   |
|---------------------------|---|-------------|---|------------------|
| 100<br>_g_<br>_at         | Y08200 /FEATURE=<br>/DEFINITION=HSRABGTRA Homo<br>sapiens mRNA for rab geranylgeranyl<br>transferase, alpha-subunit | RABG<br>GTA | Rab<br>geranylgeranyltr<br>ansferase,<br>alpha subunit  | 14q11.<br>2      |
| 105<br>2_s<br>_at         | M83667 /FEATURE=mRNA<br>/DEFINITION=HUMNFIL6BA Human<br>NF-IL6-beta protein mRNA, complete<br>cds                   | CEBP<br>D   | CCAAT/enhanc<br>er binding<br>protein (C/EBP),<br>delta | 8p11.2<br>-p11.1 |
| 106<br>2_g<br>_at         | U00672 /FEATURE=<br>/DEFINITION=U00672 Human<br>interleukin-10 receptor mRNA,<br>complete cds                       | IL10R<br>A  | interleukin 10<br>receptor, alpha                       | 11q23            |
| 109<br>6_g<br>_at         | M28170 /FEATURE=<br>/DEFINITION=HUMCSPC Human cell<br>surface protein CD19 (CD19) gene,<br>complete cds             | CD19        | CD19 antigen  | 16p11.<br>2      |
| 110<br>5_s<br>_at         | M12886 /FEATURE=<br>/DEFINITION=HUMTCBY Human T-<br>cell receptor active beta-chain mRNA,<br>complete cds           | TRB         | T cell receptor<br>beta locus                           | 7q35             |
| 111<br>0_a                | M21624 /FEATURE=mRNA<br>/DEFINITION=HUMTCRGC Human T-   | TRD         | T cell receptor<br>delta locus                          | 14q11.<br>2      |



|                   |   |            |  |                |
|-------------------|---|------------|--|----------------|
| t                 | cell receptor delta chain mRNA (VJC-region), complete cds   |            | delta locus  | 2              |
| 111<br>5_a<br>t   | M25897 /FEATURE=mRNA<br>/DEFINITION=HUMPF4A Human<br>platelet factor 4 (PF4) mRNA,<br>complete cds  | PF4        | platelet factor 4  | 4q12-<br>q21   |
| 111<br>7_a<br>t   | L27943 /FEATURE=mRNA<br>/DEFINITION=HUMCYDE Homo<br>sapiens cytidine deaminase (CDA)<br>mRNA, complete cds                                | CDA        | cytidine<br>deaminase  | 1p36.2<br>-p35 |
| 114<br>0_a<br>t   | L25851 /FEATURE=<br>/DEFINITION=HUMINAE Homo<br>sapiens integrin alpha E precursor,<br>mRNA, complete cds                                 | ITGAE      | "integrin, alpha<br>E (antigen<br>CD103, human<br>mucosal<br>lymphocyte<br>antigen 1; alpha<br>polypeptide)" | 17p13          |
| 118<br>5_a<br>t   | D49410 /FEATURE=expanded_cds<br>/DEFINITION=HUMIL3RA12 Human<br>gene for interleukin 3 receptor alpha<br>subunit, exon 12 and partial cds |            |  |                |
| 121<br>7_g<br>_at | X07109 /FEATURE=cds<br>/DEFINITION=HSPKCB2A Human<br>mRNA for protein kinase C (PKC) type<br>beta II                                      | PRKC<br>B1 | protein kinase<br>C, beta 1  | 16p11.<br>2    |
| 123<br>0_g<br>_at | U78556 /FEATURE=<br>/DEFINITION=HSU78556 Human<br>cisplatin resistance associated alpha<br>protein (hCRA alpha) mRNA, complete            | CRA        | cisplatin<br>resistance<br>associated  | 1q12-<br>q21   |

|                 |  |            |   |                         |
|-----------------|--|------------|---|-------------------------|
|                 | cds  |            |   |                         |
| 125<br>2_a<br>t | M73547 /FEATURE=<br>/DEFINITION=HUMPOLLA Human<br>polyposis locus (DP1 gene) mRNA,<br>complete cds                                       | D5S34<br>6 | DNA segment,<br>single copy<br>probe LNS-<br>CAI/LNS-CAII<br>(deleted in<br>polyposis                 | 5q22-<br>q23            |
| 137<br>_at      | U65404 /FEATURE=<br>/DEFINITION=HSU65404 Human<br>erythroid-specific transcription factor<br>EKLF mRNA, complete cds                     | KLF1       | Kruppel-like<br>factor 1<br>(erythroid)   | 19p13.<br>13-<br>p13.12 |
| 138<br>5_a<br>t | M77349 /FEATURE=<br>/DEFINITION=HUMTGFBIG Human<br>transforming growth factor-beta<br>induced gene product (BIGH3) mRNA,<br>complete cds | TGFB1      | transforming<br>growth factor,<br>beta-induced,<br>68kD   | 5q31                    |
| 138<br>9_a<br>t | J03779 /FEATURE=mRNA<br>/DEFINITION=HUMCALLA Human<br>common acute lymphoblastic leukemia<br>antigen (CALLA) mRNA, complete cds          | MME        | membrane<br>metallo-<br>endopeptidase<br>(neutral<br>endopeptidase,<br>enkephalinase,<br>CALLA, CD10) | 3q25.1<br>-q25.2        |
| 138<br>_at      | U66464 /FEATURE=<br>/DEFINITION=HSU66464 Human<br>hematopoietic progenitor kinase<br>(HPK1) mRNA, complete cds                           | MAP4<br>K1 | mitogen-<br>activated protein<br>kinase kinase<br>kinase kinase 1                                     | 19q13.<br>1-<br>q13.4   |
| 140<br>2_a<br>t | M16038 /FEATURE=<br>/DEFINITION=HUMLYN Human lyn<br>mRNA encoding a tyrosine kinase  | LYN        | v-yes-1<br>Yamaguchi<br>sarcoma viral   | 8q13                    |

|                   |  |       |  |              |
|-------------------|--|-------|--|--------------|
| t                 | mRNA encoding a tyrosine kinase  |       | related<br>oncogene<br>homolog                                       |              |
| 147<br>4_s<br>_at | U22376 /FEATURE=cds#3<br>/DEFINITION=HSU22376 Human (c-<br>myb) gene, complete primary cds, and<br>five complete alternatively spliced cds       |       |  |              |
| 147<br>6_s<br>_at | U22376 /FEATURE=cds#5<br>/DEFINITION=HSU22376 Human (c-<br>myb) gene, complete primary cds, and<br>five complete alternatively spliced cds       |       |  |              |
| 149<br>5_a<br>t   | M34057 /FEATURE=<br>/DEFINITION=HUMTGFB1B Human<br>transforming growth factor-beta 1<br>binding protein mRNA, complete cds                       | LTBP1 | latent<br>transforming<br>growth factor<br>beta binding<br>protein 1 | 2p22-<br>p21 |
| 149<br>7_a<br>t   | L04270 /FEATURE=<br>/DEFINITION=HUMTNFRRP Homo<br>sapiens (clone CD18) tumor necrosis<br>factor receptor 2 related protein<br>mRNA, complete cds | LTBR  | lymphotoxin<br>beta receptor<br>(TNFR<br>superfamily,<br>member 3)   | 12p13        |
| 149<br>8_a<br>t   | L05148 /FEATURE=<br>/DEFINITION=HUMTYRKIN Human<br>protein tyrosine kinase related mRNA<br>sequence  |       |  |              |
| 152<br>9_a<br>t   | U50534 /FEATURE=<br>/DEFINITION=HSU50534 Human<br>BRCA2 region, mRNA sequence<br>CG003   |       |  |              |

|                   |  |             |   |                  |
|-------------------|--|-------------|---|------------------|
| 163<br>6_g<br>_at | U07563 /FEATURE=Poly_A_Site#1<br>/DEFINITION=HSABLGR3 Human<br>proto-oncogene tyrosine-protein kinase<br>(ABL) gene, exon 1a and exons 2-10,<br>complete cds   |             |   |                  |
| 175<br>2_a<br>t   | AD000092 /FEATURE=cds#6<br>/DEFINITION=CH19HHR23 Homo<br>sapiens DNA from chromosome<br>19p13.2 cosmids R31240, R30272 and<br>R28549 containing the EKLF, GCDH,<br>CRTC, and RAD23A genes, genomic<br>sequence |             |   |                  |
| 188<br>4_s<br>_at | M15796 /FEATURE=<br>/DEFINITION=HUMCYL Human cyclin<br>protein gene, complete cds  | PCNA        | proliferating cell<br>nuclear antigen                         | 20pter-<br>p12   |
| 191<br>1_s<br>_at | M60974 /FEATURE=<br>/DEFINITION=HUMGADD45 Human<br>growth arrest and DNA-damage-<br>inducible protein (gadd45) mRNA,<br>complete cds   | GADD<br>45A | growth arrest<br>and DNA-<br>damage-<br>inducible, alpha      | 1p31.2<br>-p31.1 |
| 195<br>9_a<br>t   | D88674 /FEATURE=<br>/DEFINITION=D88674 Homo sapiens<br>mRNA for antizyme inhibitor, complete<br>cds  | OAZIN       | ornithine<br>decarboxylase<br>antizyme<br>inhibitor           | 8q22.3           |
| 198<br>0_s<br>_at | X58965 /FEATURE=<br>/DEFINITION=HSNM23H2G H.sapiens<br>RNA for nm23-H2 gene  | NME2        | non-metastatic<br>cells 2, protein<br>(NM23B)<br>expressed in | 17q21.<br>3      |
| 198<br>3_a        | X68452 /FEATURE=cds<br>/DEFINITION=HSCYCD2 H.sapiens   | CCND<br>2   | cyclin D2   | 12p13            |

|                   |  |       |   |                |
|-------------------|--|-------|---|----------------|
| t                 | mRNA for cyclin D2   | 2     |   |                |
| 201<br>9_s<br>_at | M68892 /FEATURE=<br>/DEFINITION=HUMINTB7 Human<br>integrin beta-7 subunit mRNA,<br>complete cds  | ITGB7 | integrin, beta 7  | 12q13.<br>13   |
| 202<br>4_s<br>_at | M79321 /FEATURE=<br>/DEFINITION=HUMLYNTK Human<br>Lyn B protein mRNA, complete cds   | LYN   | v-yes-1<br>Yamaguchi<br>sarcoma viral<br>related<br>oncogene<br>homolog | 8q13           |
| 204<br>2_s<br>_at | M15024 /FEATURE=<br>/DEFINITION=HUMCMYBLA Human<br>c-myb mRNA, complete cds  | MYB   | v-myb avian<br>myeloblastosis<br>viral oncogene<br>homolog              | 6q22-<br>q23   |
| 204<br>5_s<br>_at | M16592 /FEATURE=mRNA<br>/DEFINITION=HUMHCKB Human<br>hemopoietic cell protein-tyrosine<br>kinase (HCK) gene, complete cds,<br>clone HK24 | HCK   | hemopoietic cell<br>kinase  | 20q11-<br>q12  |
| 204<br>7_s<br>_at | M23410 /FEATURE=<br>/DEFINITION=HUMPLAKO Human<br>plakoglobin (PLAK) mRNA, complete<br>cds   | JUP   | junction<br>plakoglobin   | 17q21          |
| 205<br>9_s<br>_at | M36881 /FEATURE=mRNA<br>/DEFINITION=HUMLCKAA Human<br>lymphocyte-specific protein tyrosine<br>kinase (lck) mRNA, complete cds            | LCK   | lymphocyte-<br>specific protein<br>tyrosine kinase                      | 1p35-<br>p34.3 |

|                   |   |            |   |                       |
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| 206<br>9_s<br>_at | L23805<br>/FEATURE=<br>/DEFINITION=HUMCATENIN Human<br>alpha1(E)-catenin mRNA, complete<br>cds  | CTNN<br>A1 | catenin<br>(cadherin-<br>associated<br>protein), alpha 1<br>(102kD) | 5q31                  |
| 210<br>_at        | M95678<br>/FEATURE=<br>/DEFINITION=HUMPLCB2A Homo<br>sapiens phospholipase C-beta-2<br>mRNA, complete cds   | PLCB2      | phospholipase<br>C, beta 2  | 15q15                 |
| 245<br>_at        | M25280<br>/FEATURE=<br>/DEFINITION=HUMLNHR Human<br>lymph node homing receptor mRNA,<br>complete cds  | SELL       | selectin L<br>(lymphocyte<br>adhesion<br>molecule 1)                | 1q23-<br>q25          |
| 256<br>_s_<br>_at | M14199<br>/FEATURE=<br>/DEFINITION=HUMLAMR Human<br>laminin receptor (2H5 epitope) mRNA,<br>5 end   | LAMR<br>1  | laminin receptor<br>1 (67kD,<br>ribosomal<br>protein SA)            | 3p21.3                |
| 277<br>_at        | L08246<br>/FEATURE=<br>/DEFINITION=HUMMCL1X Human<br>myeloid cell differentiation protein<br>(MCL1) mRNA  |            |   |                       |
| 307<br>_at        | J03600<br>/FEATURE=<br>/DEFINITION=HUMLOX5 Human<br>lipoxygenase mRNA, complete cds   | ALOX5      | arachidonate 5-<br>lipoxygenase                                     | 10q11.<br>2           |
| 313<br>81_<br>_at | Cluster Incl. AF076483:Homo sapiens<br>peptidoglycan recognition protein<br>precursor (PGRP) mRNA, complete<br>cds /cds=(44,634) /gb=AF076483<br>/gi=3342532 /ug=Hs.137583 /len=690 | PGLY<br>RP | peptidoglycan<br>recognition<br>protein                             | 19q13.<br>2-<br>q13.3 |

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| 317<br>93_<br>at   | Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end<br>/clone=DKFZp564J2262 /clone_end=5<br>/gb=AL036554 /gi=5927801<br>/ug=Hs.1379 /len=517 | DEFA3    | defensin, alpha 3, neutrophil-specific   | 8pter-p23.3   |
| 318<br>59_<br>at   | Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds<br>/cds=(19,2142) /gb=J05070<br>/gi=177204 /ug=Hs.151738 /len=2334                      | MMP9     | matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) | 20q11.2-q13.1 |
| 318<br>70_<br>at   | Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908)<br>/gb=X14046 /gi=29793 /ug=Hs.153053<br>/len=1125                               | CD37     | CD37 antigen   | 19p13-q13.4   |
| 318<br>98_<br>at   | Cluster Incl. D86967:Human mRNA for KIAA0212 gene, complete cds<br>/cds=(58,2031) /gb=D86967<br>/gi=1504007 /ug=Hs.154332 /len=6072                       | KIAA0212 | KIAA0212 gene product  | 3p25.3        |
| 319<br>36_<br>s_at | Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds<br>/cds=(0,3172) /gb=AB007890<br>/gi=2887438 /ug=Hs.166163 /len=6011                      | KIAA0430 | KIAA0430 gene product  | 16p13.12      |
| 320<br>72_<br>at   | Cluster Incl. U40434:Human mesothelin or CAK1 antigen precursor mRNA, complete cds /cds=(99,1985)<br>/gb=U40434 /gi=1145723<br>/ug=Hs.155981 /len=2114    | MSLN     | mesothelin   | 16p13.3       |

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| 320<br>80_<br>at | Cluster Incl. L11669:Human<br>tetracycline transporter-like protein<br>mRNA, complete cds /cds=(120,1487)<br>/gb=L11669 /gi=307501<br>/ug=Hs.157145 /len=1758                      | TETR<br>AN   | tetracycline<br>transporter-like<br>protein   | 4p16.3      |
| 321<br>45_<br>at | Cluster Incl. X58141:Human mRNA for<br>erythrocyte adducin alpha subunit<br>/cds=(154,2367) /gb=X58141<br>/gi=28381 /ug=Hs.183706 /len=3905  |              |   |             |
| 321<br>66_<br>at | Cluster Incl. AB028950:Homo sapiens<br>mRNA for KIAA1027 protein, partial<br>cds /cds=(0,5088) /gb=AB028950<br>/gi=5689390 /ug=Hs.18420 /len=5542                                  | TLN1         | talin 1   | 9p13        |
| 321<br>74_<br>at | Cluster Incl. AF015926:Homo sapiens<br>ezrin-radixin-moesin binding<br>phosphoprotein-50 mRNA, complete<br>cds /cds=(212,1288) /gb=AF015926<br>/gi=3220018 /ug=Hs.184276 /len=1984 | SLC9A<br>3R1 | solute carrier<br>family 9<br>(sodium/hydrog<br>en exchanger),<br>isoform 3<br>regulatory factor<br>1 | 17q25.<br>2 |
| 321<br>84_<br>at | Cluster Incl. X61118:Human TTG-2<br>mRNA for a cysteine rich protein with<br>LIM motif /cds=UNKNOWN<br>/gb=X61118 /gi=663012<br>/ug=Hs.184585 /len=2292                            | LMO2         | LIM domain only<br>2 (rhombotin-<br>like 1)   | 11p13       |
| 322<br>29_<br>at | Cluster Incl. AF038957:Homo sapiens<br>translation initiation factor 4e mRNA,<br>complete cds /cds=(58,768)<br>/gb=AF038957 /gi=3329383<br>/ug=Hs.19122 /len=961                   | EIF4E<br>L3  | eukaryotic<br>translation<br>initiation factor<br>4E-like 3   | 2q37.1      |



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| 322<br>32_<br>at | Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034             | NDUF<br>B5 | NADH<br>dehydrogenase<br>(ubiquinone) 1<br>beta<br>subcomplex, 5<br>(16kD, SGD)       | 3q27.1                |
| 322<br>59_<br>at | Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gi=2224716 /ug=Hs.194669 /len=4606   | EZH1       | enhancer of<br>zeste<br>(Drosophila)<br>homolog 1                                     | 17q21.<br>1-<br>q21.3 |
| 323<br>19_<br>at | Cluster Incl. AL022310:dJ395P12.2 (tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L)) /cds=(137,688) /gb=AL022310 /gi=3646083 /ug=Hs.181097 /len=3470 |            |   |                       |
| 323<br>23_<br>at | Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457   |            |   |                       |
| 324<br>34_<br>at | Cluster Incl. D10522:Homo sapiens mRNA for 80K-L protein, complete cds /cds=(369,1367) /gb=D10522 /gi=219893 /ug=Hs.75607 /len=2589  | MACS       | myristoylated<br>alanine-rich<br>protein kinase C<br>substrate<br>(MARCKS, 80K-<br>L) | 6q22.2                |
| 325<br>06_<br>at | Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576                                       | TBC1<br>D1 | TBC1 (tre-<br>2/USP6, BUB2,<br>cdc16) domain<br>family, member<br>1                   | 4                     |

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| 325<br>30_<br>at | Cluster Incl. X56468:Human mRNA for 14.3.3 protein, a protein kinase regulator /cds=(125,862) /gb=X56468 /gi=23221 /ug=Hs.74405 /len=1862 | YWHA<br>Q | tyrosine 3-monooxygenase /tryptophan 5-monooxygenase activation protein, theta polypeptide | 22q12-qter    |
| 325<br>43_<br>at | Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937       | CALR      | calreticulin   | 19p13.3-p13.2 |
| 325<br>97_<br>at | Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835                     | RBL2      | retinoblastoma-like 2 (p130)   | 16q12.2       |
| 326<br>16_<br>at | Cluster Incl. M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(297,1835) /gb=M16038 /gi=187268 /ug=Hs.80887 /len=2298               | LYN       | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog                                   | 8q13          |
| 326<br>49_<br>at | Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910      | TCF7      | transcription factor 7 (T-cell specific, HMG-box)  | 5q31.1        |
| 326<br>96_<br>at | Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314 /ug=Hs.171680 /len=2581  | PBX3      | pre-B-cell leukemia transcription  | 9q33-q34      |

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| at                 | /gi=35314 /ug=Hs.171680 /len=2581   |         | factor 3  |          |
| 327<br>06_<br>at   | Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cds=(220,3273) /gb=X89887 /gi=3928218 /ug=Hs.172350 /len=4018                        | HIRA    | HIR (histone cell cycle regulation defective) homolog A (S. cerevisiae) | 22q11.21 |
| 327<br>47_<br>at   | Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase I ALDH I (EC 1.2.1.3) /cds=(36,1586) /gb=X05409 /gi=28605 /ug=Hs.195432 /len=1989 | ALDH2   | aldehyde dehydrogenase 2 family (mitochondrial)                         | 12q24.2  |
| 327<br>75_<br>r_at | Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077                          | PLSC R1 | phospholipid scramblase 1   | 3q23     |
| 328<br>00_<br>at   | Cluster Incl. U66306:Human retinoid X receptor alpha mRNA, 3 UTR, partial sequence /cds=UNKNOWN /gb=U66306 /gi=3411007 /ug=Hs.20084 /len=3772             |         |   |          |
| 328<br>19_<br>at   | Cluster Incl. AJ223352:Homo sapiens mRNA for histone H2B, clone pjG4-5-14 /cds=(16,396) /gb=AJ223352 /gi=3255996 /ug=Hs.20418 /len=793                    | H2BFA   | H2B histone family, member A  | 6p21.3   |
| 328<br>21_<br>at   | Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677              | LCN2    | lipocalin 2 (oncogene 24p3)   | 9q34     |

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| 328<br>42_<br>at       | Cluster Incl. X89984:H.sapiens mRNA for BCL7A protein /cds=(953,1648) /gb=X89984 /gi=929614 /ug=Hs.211563 /len=4522  | BCL7A | B-cell CLL/lymphoma 7A               | 12q24.13      |
| 331<br>02_<br>at       | Cluster Incl. D67031:Homo sapiens ADDL mRNA for adducin-like protein, complete cds /cds=(183,2207) /gb=D67031 /gi=2696053 /ug=Hs.8110 /len=2920                              | ADD3  | adducin (gamma) 3                    | 10q24.2-q24.3 |
| 331<br>21_<br>g_a<br>t | Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753                     | RGS10 | regulator of G-protein signalling 10 | 10q25         |
| 331<br>34_<br>at       | Cluster Incl. AB011083:Homo sapiens mRNA for KIAA0511 protein, partial cds /cds=(0,2802) /gb=AB011083 /gi=3043545 /ug=Hs.8402 /len=3563                                      | ADCY3 | adenylate cyclase 3                  | 2p24-p22      |
| 332<br>38_<br>at       | Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinase p56lck (lck) abberant mRNA, complete cds /cds=(59,1150) /gb=U23852 /gi=775207 /ug=Hs.1765 /len=2129 |       |                                      |               |
| 332<br>66_<br>at       | Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRNA, complete cds /cds=(58,1101) /gb=AF015254 /gi=4090840 /ug=Hs.180655 /len=1234                       | STK12 | serine/threonine kinase 12           | 17p13.1       |

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| 332<br>73_<br>f_at | Cluster Incl. X57809:Human<br>rearranged immunoglobulin lambda<br>light chain mRNA /cds=(114,815)<br>/gb=X57809 /gi=33714 /ug=Hs.181125<br>/len=915   | IGL          | immunoglobulin<br>lambda locus        | 22q11.<br>1-<br>q11.2 |
| 332<br>74_<br>f_at | Cluster Incl. M18645:Human Ig<br>rearranged lambda-chain mRNA VJC-<br>region subgroup lambda-IV from<br>heterohybridoma H6-3C4<br>/cds=(30,731) /gb=M18645 /gi=186103<br>/ug=Hs.181125 /len=872 | IGL          | immunoglobulin<br>lambda locus        | 22q11.<br>1-<br>q11.2 |
| 332<br>84_<br>at   | Cluster Incl. M19507:Human<br>myeloperoxidase mRNA, complete cds<br>/cds=UNKNOWN /gb=M19507<br>/gi=188657 /ug=Hs.1817 /len=3215   | MPO          | myeloperoxidas<br>e                   | 17q23.<br>1           |
| 333<br>19_<br>at   | Cluster Incl. AF009674:Homo sapiens<br>axin (AXIN) mRNA, partial cds<br>/cds=(0,2703) /gb=AF009674<br>/gi=2252819 /ug=Hs.184434 /len=3385   | AXIN1        | axin                                  | 16p13.<br>3           |
| 333<br>51_<br>at   | Cluster Incl. AF064607:Homo sapiens<br>GC20 protein mRNA, complete cds<br>/cds=(70,411) /gb=AF064607<br>/gi=3152667 /ug=Hs.21756 /len=812   | GC20         | translation<br>factor sui1<br>homolog | 3p21.3<br>3           |
| 333<br>52_<br>at   | Cluster Incl. X57985:H.sapiens genes<br>for histones H2B.1 and H2A<br>/cds=(42,422) /gb=X57985 /gi=510989<br>/ug=Hs.2178 /len=2223  |              |                                       |                       |
| 333<br>58_<br>at   | Cluster Incl. W29087:56b8 Homo<br>sapiens cDNA /gb=W29087<br>/gi=1309053 /ug=Hs.21894 /len=877  | KIAA1<br>157 | KIAA1157<br>protein                   | 12q13.<br>3-<br>q14.1 |

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| at                 | /gi=1309053 /ug=Hs.21894 /len=877   |            |  | q14.1    |
| 333<br>71_<br>s_at | Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907  | RAB31      | RAB31, member RAS oncogene family                    | 18p11.3  |
| 333<br>86_<br>at   | Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome 22q12-13 Contains H1F0(H1 histone family, member 0) gene, 2-amino-3-ketobutyrate -CoA ligase( nuclear gene encoding mitochondrial protein), GALR3 (galanin receptor) gene, ESTs, GSSs an |            |  |          |
| 333<br>90_<br>at   | Cluster Incl. AA203487:zx53d03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446213 /clone_end=5 /gb=AA203487 /gi=1799460 /ug=Hs.226237 /len=863   |            | ESTs   |          |
| 334<br>12_<br>at   | Cluster Incl. AI535946:vicpro2.D07.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI535946 /gi=4450081 /ug=Hs.227751 /len=647  | LGALS<br>1 | lectin, galactoside-binding, soluble, 1 (galectin 1) | 22q13.1  |
| 334<br>14_<br>at   | Cluster Incl. X57398:Human mRNA for pM5 protein /cds=(0,3572) /gb=X57398 /gi=35526 /ug=Hs.227823 /len=4086  | PM5        | pM5 protein  | 16p13.11 |
| 334<br>25_<br>at   | Cluster Incl. X97548:H.sapiens mRNA for TIF1beta zinc finger protein /cds=(361,2868) /gb=X97548 /gi=1524108 /ug=Hs.228059 /len=3035   | TRIM2<br>8 | tripartite motif-containing 28                       | 5        |

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|                    | /gi=1524108 /ug=Hs.228059 /len=3035  |             |   |                  |
| 334<br>41_<br>at   | "Cluster Incl. L41143:Homo sapiens<br>expressed pseudo TCTA mRNA at<br>t(1;3) translocation site, complete cds<br>/cds=(221,532) /gb=L41143<br>/gi=736684 /ug=Hs.232069 /len=2146" |             |   |                  |
| 334<br>54_<br>at   | Cluster Incl. AF016903:Homo sapiens<br>agrin precursor mRNA, partial cds<br>/cds=(0,6080) /gb=AF016903<br>/gi=2988421 /ug=Hs.234137 /len=7032                                      | AGRN        | agrin   | 1p36.3<br>-p32   |
| 335<br>30_<br>at   | Cluster Incl. M33326:Human<br>nonspecific cross-reacting antigen<br>(NCA) mRNA, complete cds<br>/cds=(86,1135) /gb=M33326<br>/gi=189101 /ug=Hs.41 /len=2287                        | CEAC<br>AM8 | carcinoembryoni<br>c antigen-<br>related cell<br>adhesion<br>molecule 8                       | 19q13.<br>2      |
| 336<br>89_<br>s_at | Cluster Incl. AF012434:untitled<br>/cds=(38,394) /gb=AF012434<br>/gi=2352914 /ug=Hs.186570 /len=573  |             |   |                  |
| 337<br>31_<br>at   | Cluster Incl. AJ130718:Homo sapiens<br>mRNA for glycoprotein-associated<br>amino acid transporter y+LAT1<br>/cds=(293,1828) /gb=AJ130718<br>/gi=3970724 /ug=Hs.194693 /len=2214    | SLC7A<br>7  | solute carrier<br>family 7<br>(cationic amino<br>acid transporter,<br>y+ system),<br>member 7 | 14q11.<br>2      |
| 337<br>52_<br>at   | Cluster Incl. AB020657:Homo sapiens<br>mRNA for KIAA0850 protein, complete<br>cds /cds=(630,2558) /gb=AB020657<br>/gi=4240188 /ug=Hs.197298 /len=3682                              | NS1-<br>BP  | NS1-binding<br>protein  | 1q25.1<br>-q31.1 |

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| 338<br>12_<br>at | "Cluster Incl. AL049415:Homo sapiens mRNA; cDNA DKFZp586N2119 (from clone DKFZp586N2119) /cds=UNKNOWN /gb=AL049415 /gi=4500196 /ug=Hs.204290 /len=1232"   |          |                                     |         |
| 338<br>21_<br>at | Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL |          |                                     |         |
| 338<br>56_<br>at | Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protein /cds=(343,972) /gb=Y13374 /gi=2370152 /ug=Hs.239533 /len=1186  | CXX1     | CAAX box 1                          | Xq26    |
| 338<br>60_<br>at | Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150   | KIAA0462 | KIAA0462 protein                    | 1p36.13 |
| 338<br>66_<br>at | Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049   | TPM4     | tropomyosin 4                       | 19p13.1 |
| 339<br>05_<br>at | Cluster Incl. AF072242:Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds /cds=(229,1464) /gb=AF072242  | MBD2     | methyl-CpG binding domain protein 2 | 18q21   |



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|                        | /gi=3800792 /ug=Hs.25674 /len=1948   |              |  |           |
| 339<br>20_<br>at       | Cluster Incl. AF051782:Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds /cds=(0,3746) /gb=AF051782 /gi=2947237 /ug=Hs.26584 /len=5635                | DIAPH<br>1   | diaphanous (Drosophila, homolog) 1         | 5q31      |
| 339<br>24_<br>at       | Cluster Incl. AB029014:Homo sapiens mRNA for KIAA1091 protein, partial cds /cds=(0,4080) /gb=AB029014 /gi=5689518 /ug=Hs.26797 /len=4248                 | KIAA1<br>091 | KIAA1091 protein                           | 11        |
| 339<br>44_<br>at       | Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727 | APLP2        | amyloid beta (A4) precursor-like protein 2 | 11q24     |
| 339<br>63_<br>at       | Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771) /gb=M96326 /gi=179301 /ug=Hs.72885 /len=913                                       |              |  |           |
| 341<br>10_<br>g_a<br>t | Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888                   | PIG6         | proline oxidase homolog                    |           |
| 341<br>68_<br>at       | Cluster Incl. M11722:Human terminal transferase mRNA, complete cds /cds=(328,1854) /gb=M11722 /gi=339436 /ug=Hs.234772 /len=2068                         | DNTT         | deoxynucleotidyltransferase, terminal      | 10q23-q24 |
| 342<br>10_             | Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end   | CDW5<br>2    | CDW52 antigen (CAMPATH-1                   | 1p36      |

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| at               | /clone=IMAGE-301723 /clone_end=3<br>/gb=N90866 /gi=1444193<br>/ug=Hs.214742 /len=577   | 2          | antigen)  |               |
| 342<br>51_<br>at | Cluster Incl. M92299:Human<br>homeobox 2.1 protein (HOX2A)<br>mRNA, complete cds /cds=(275,1084)<br>/gb=M92299 /gi=184292 /ug=Hs.22554<br>/len=2037                | HOXB<br>5  | homeo box B5  | 17q21-<br>q22 |
| 343<br>06_<br>at | Cluster Incl. AB007888:Homo sapiens<br>KIAA0428 mRNA, complete cds<br>/cds=(1414,2526) /gb=AB007888<br>/gi=2887430 /ug=Hs.28578 /len=5940                          | MBNL       | muscleblind<br>(Drosophila)-like  | 3q25          |
| 343<br>62_<br>at | Cluster Incl. M55531:Human glucose<br>transport-like 5 (GLUT5) mRNA,<br>complete cds /cds=(75,1580)<br>/gb=M55531 /gi=183297 /ug=Hs.33084<br>/len=2218             | SLC2A<br>5 | solute carrier<br>family 2<br>(facilitated<br>glucose/fructose<br>transporter),<br>member 5 | 1p36.2        |
| 343<br>67_<br>at | Cluster Incl. AF006043:Homo sapiens<br>3-phosphoglycerate dehydrogenase<br>mRNA, complete cds /cds=(692,2293)<br>/gb=AF006043 /gi=2674061<br>/ug=Hs.3343 /len=2467 | PHGD<br>H  | phosphoglycerat<br>e<br>dehydrogenase   | 1p12          |
| 345<br>12_<br>at | Cluster Incl. J03853:Human kidney<br>alpha-2-adrenergic receptor mRNA,<br>complete cds /cds=(38,1423)<br>/gb=J03853 /gi=178193<br>/ug=Hs.123022 /len=1491          | ADRA<br>2C | adrenergic,<br>alpha-2C-,<br>receptor   | 4p16          |
| 345<br>46_       | Cluster Incl. AI250799:qi36g07.x1<br>Homo sapiens cDNA, 3 end  | DEFA4      | defensin, alpha<br>4, corticostatin   | 8p23          |

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| at               | /clone=IMAGE-1858620 /clone_end=3<br>/gb=AI250799 /gi=3847328<br>/ug=Hs.2582 /len=542  |            | 4, corticostatin   |              |
| 345<br>83_<br>at | Cluster Incl. U02687:Human growth<br>factor receptor tyrosine kinase (STK-1)<br>mRNA, complete cds /cds=(57,3038)<br>/gb=U02687 /gi=409572 /ug=Hs.385<br>/len=3475           | FLT3       | fms-related<br>tyrosine kinase<br>3                                | 13q12        |
| 346<br>54_<br>at | Cluster Incl. AJ224979:Homo sapiens<br>mRNA for MTMR1 protein<br>/cds=(0,1990) /gb=AJ224979<br>/gi=4128155 /ug=Hs.23200 /len=2582  | MTMR<br>1  | myotubularin<br>related protein 1                                  | Xq28         |
| 346<br>63_<br>at | Cluster Incl. M28696:Human low-<br>affinity IgG Fc receptor (beta-Fc-<br>gamma-RII) mRNA, complete cds<br>/cds=(41,916) /gb=M28696 /gi=184843<br>/ug=Hs.233450 /len=1416     | FCGR<br>2B | Fc fragment of<br>IgG, low affinity<br>IIb, receptor for<br>(CD32) | 1q23         |
| 346<br>70_<br>at | Cluster Incl. U60899:Human lysosomal<br>alpha-mannosidase (manB) gene<br>/cds=(309,3341) /gb=U60899<br>/gi=2209014 /ug=Hs.234070 /len=3443                                   |            |  |              |
| 346<br>79_<br>at | Cluster Incl. X02596:Human mRNA for<br>bcr (breakpoint cluster region) gene in<br>Philadelphia chromosome<br>/cds=(488,4303) /gb=X02596<br>/gi=29420 /ug=Hs.234799 /len=4739 | BCR        | breakpoint<br>cluster region                                       | 22q11.<br>23 |
| 347<br>80_<br>at | Cluster Incl. AB002313:Human mRNA<br>for KIAA0315 gene, partial cds<br>/cds=(0,5526) /gb=AB002313<br>/gi=2280475 /ug=Hs.3989 /len=6252                                       | PLXN<br>B2 | plexin B2  | 22q13.<br>33 |

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|                  | /gi=2280475 /ug=Hs.3989 /len=6252  |               |   |          |
| 347<br>85_<br>at | Cluster Incl. AB028948:Homo sapiens mRNA for KIAA1025 protein, partial cds /cds=(0,3441) /gb=AB028948 /gi=5689386 /ug=Hs.4084 /len=6131  | KIAA1025      | KIAA1025 protein  | 12q24.22 |
| 347<br>89_<br>at | Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072 /len=1465 | SERPINB6      | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6                    | 6p25     |
| 348<br>30_<br>at | Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769  | DKFZP564K0822 | hypothetical protein DKFZp564K0822  | 6        |
| 348<br>71_<br>at | Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614  |               | Homo sapiens cDNA FLJ11714 fis, clone HEMBA100521 9, weakly similar to NUCLEAR PROTEIN SNF7 |          |
| 348<br>92_<br>at | Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds /cds=(117,1439) /gb=AF016266 /gi=2529562 /ug=Hs.51233 /len=3972  | TNFRSF10B     | tumor necrosis factor receptor superfamily, member 10b                                      | 8p22-p21 |
| 350<br>16_<br>at | Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080   |               |   |          |

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|                  | /gi=184518 /ug=Hs.84298 /len=2080   |             |  |                 |
| 350<br>78_<br>at | Cluster Incl. X93093:H.sapiens LW<br>gene /cds=(9,824) /gb=X93093<br>/gi=1491707 /ug=Hs.108287 /len=1243  | ICAM4       | intercellular<br>adhesion<br>molecule 4,<br>Landsteiner-<br>Wiener blood<br>group  | 19p13.<br>2-cen |
| 351<br>54_<br>at | Cluster Incl. W68046:zd42a12.s1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-343294 /clone_end=3<br>/gb=W68046 /gi=1376935<br>/ug=Hs.25817 /len=575  | BTBD2       | BTB (POZ)<br>domain<br>containing 2  | 19p13.<br>3     |
| 352<br>04_<br>at | Cluster Incl. U52840:Homo sapiens<br>semaphorin F homolog mRNA,<br>complete cds /cds=(637,3861)<br>/gb=U52840 /gi=2772583<br>/ug=Hs.27621 /len=8056 | SEMA<br>5A  | sema domain,<br>seven<br>thrombospondin<br>repeats (type 1<br>and type 1-like),<br>transmembrane<br>domain (TM)<br>and short<br>cytoplasmic<br>domain,<br>(semaphorin)<br>5A | 5p15.2          |
| 352<br>30_<br>at | Cluster Incl. AF070530:Homo sapiens<br>clone 24751 unknown mRNA<br>/cds=(0,1252) /gb=AF070530<br>/gi=3387885 /ug=Hs.29344 /len=1560                 | CL247<br>51 | hypothetical<br>protein, clone<br>24751  | 19p13.<br>3     |
| 352<br>60_<br>at | Cluster Incl. AB020674:Homo sapiens<br>mRNA for KIAA0867 protein, complete<br>cds /cds=(152,1732) /gb=AB020674                                      | MOND<br>OA  | KIAA0867<br>protein  | 12q21.<br>31    |

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| at                 | /gi=4240222 /ug=Hs.52081 /len=4339   |               |   |             |
| 352<br>64_<br>at   | Cluster Incl. AF067139:Homo sapiens NADH-ubiquinone oxidoreductase NDUF S3 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds /cds=(12,806) /gb=AF067139 /gi=3337440 /ug=Hs.5273 /len=887 | NDUF S3       | NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) | 11p11.11    |
| 352<br>82_<br>r_at | Cluster Incl. M33680:Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds /cds=(238,948) /gb=M33680 /gi=338677 /ug=Hs.54457 /len=1480   | CD81          | CD81 antigen (target of antiproliferative antibody 1)                             | 11p15       |
| 353<br>29_<br>at   | Cluster Incl. AF091084:Homo sapiens clone 638 unknown mRNA, complete sequence /cds=(30,413) /gb=AF091084 /gi=3860005 /ug=Hs.5825 /len=1065   | LOC51706      | cytochrome b5 reductase 1 (B5R.1)   | 1p36.13-q41 |
| 353<br>40_<br>at   | Cluster Incl. A1819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409932 /clone_end=3 /gb=A1819948 /gi=5439027 /ug=Hs.5947 /len=569   | MEL           | mel transforming oncogene (derived from cell line NK14)-RAB8 homolog              | 19p13.1     |
| 353<br>50_<br>at   | Cluster Incl. AB011170:Homo sapiens mRNA for KIAA0598 protein, complete cds /cds=(581,2266) /gb=AB011170 /gi=3043719 /ug=Hs.6079 /len=4712   | GALN AC4S-6ST | B cell RAG associated protein   | 10q26       |
| 353<br>55_         | Cluster Incl. AB020697:Homo sapiens mRNA for KIAA0890 protein, complete  | DDX30         | DEAD/H (Asp-Glu-Ala-  | 3p21.31     |

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| at                 | cds /cds=(143,3727) /gb=AB020697<br>/gi=4240268 /ug=Hs.6141 /len=3800  |             | Asp/His) box<br>polypeptide 30  | 1            |
| 353<br>72_<br>r_at | Cluster Incl. M17017:Human beta-thromboglobulin-like protein mRNA, complete cds /cds=(90,389) /gb=M17017 /gi=179579 /ug=Hs.624 /len=1639   | IL8         | interleukin 8   | 4q13-q21     |
| 356<br>38_<br>at   | Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460               | CBFA2<br>T1 | "core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related" | 8q22         |
| 356<br>43_<br>at   | Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2706486 /ug=Hs.3164 /len=1586                          | NUCB<br>2   | nucleobindin 2  | 11p15.1-p14  |
| 357<br>66_<br>at   | Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343) /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412                       | KRT18       | keratin 18  | 12q13        |
| 358<br>13_<br>at   | Cluster Incl. AA192359:zp91c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-627574 /clone_end=3 /gb=AA192359 /gi=1781699 /ug=Hs.69235 /len=715 | TRN-SR      | transportin-SR  | 7q32.2-q32.3 |
| 358<br>23_<br>at   | Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671)                                      | PPIB        | peptidylprolyl isomerase B (cyclophilin B)  | 15q21-q22    |

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| at                 | /gb=M63573 /gi=337998 /ug=Hs.699<br>/len=893  |            | (cyclophilin B)  |                 |
| 359<br>19_<br>at   | Cluster Incl. J05068:human<br>transcobalamin I mRNA, complete cds<br>/cds=(75,1376) /gb=J05068<br>/gi=307478 /ug=Hs.2012 /len=1537                                    | TCN1       | transcobalamin I<br>(vitamin B12<br>binding protein,<br>R binder family) | 11q11-<br>q12   |
| 359<br>39_<br>s_at | Cluster Incl. L20433:Human octamer<br>binding transcription factor 1 (OTF1)<br>mRNA, complete cds /cds=(234,1496)<br>/gb=L20433 /gi=418015<br>/ug=Hs.211588 /len=3824 | POU4<br>F1 | POU domain,<br>class 4,<br>transcription<br>factor 1                     | 13q21.<br>1-q22 |
| 359<br>40_<br>at   | Cluster Incl. X64624:H.sapiens mRNA<br>for RDC-1 POU domain containing<br>protein /cds=(277,1272) /gb=X64624<br>/gi=35914 /ug=Hs.211588 /len=3492                     | POU4<br>F1 | POU domain,<br>class 4,<br>transcription<br>factor 1                     | 13q21.<br>1-q22 |
| 359<br>41_<br>f_at | Cluster Incl. U91329:Human kinesin-<br>like motor protein KIF1C mRNA,<br>complete cds /cds=(113,3424)<br>/gb=U91329 /gi=2738148<br>/ug=Hs.211611 /len=4058            | KIF1C      | kinesin family<br>member 1C  | 17p13           |
| 359<br>95_<br>at   | Cluster Incl. AF067656:Homo sapiens<br>ZW10 interactor Zwint mRNA,<br>complete cds /cds=(24,857)<br>/gb=AF067656 /gi=3901271<br>/ug=Hs.42650 /len=1639                | ZWINT      | ZW10 interactor  | 10q21-<br>q22   |
| 360<br>21_<br>at   | "Cluster Incl. AL049409:Homo sapiens<br>mRNA; cDNA DKFZp586H0919 (from<br>clone DKFZp586H0919)<br>/cds=UNKNOWN /gb=AL049409   |            |  |                 |



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|                  | /gi=4500194 /ug=Hs.44865 /len=1419"  |                       |   |                  |
| 360<br>95_<br>at | Cluster Incl. N99340:IMAGE-20074<br>Homo sapiens cDNA /clone=IMAGE-<br>20074 /gb=N99340 /gi=1270755<br>/ug=Hs.7357 /len=1110   | DKFZ<br>P586N<br>1922 | DKFZP586N192<br>2 protein   | 19q13.<br>1      |
| 361<br>03_<br>at | Cluster Incl. D90144:Homo sapiens<br>gene for LD78 alpha precursor,<br>complete cds /cds=(86,364)<br>/gb=D90144 /gi=219905 /ug=Hs.73817<br>/len=781                  | SCYA<br>3             | small inducible<br>cytokine A3<br>(homologous to<br>mouse Mip-1a) | 17q11-<br>q21    |
| 361<br>23_<br>at | Cluster Incl. D87292:Homo sapiens<br>mRNA for rhodanese, complete cds<br>/cds=(48,941) /gb=D87292<br>/gi=1877030 /ug=Hs.74097 /len=1137                              | TST                   | thiosulfate<br>sulfurtransferas<br>e (rhodanese)                  | 22q13.<br>1      |
| 361<br>39_<br>at | "Cluster Incl. AL050289:Homo sapiens<br>mRNA; cDNA DKFZp586G0522 (from<br>clone DKFZp586G0522)<br>/cds=(179,1876) /gb=AL050289<br>/gi=4886510 /ug=Hs.7446 /len=2364" | C6orf5                | chromosome 6<br>open reading<br>frame 5                           | 6q21             |
| 361<br>55_<br>at | Cluster Incl. D87465:Human mRNA for<br>KIAA0275 gene, complete cds<br>/cds=(316,1590) /gb=D87465<br>/gi=1665814 /ug=Hs.74583 /len=5316                               | KIAA0<br>275          | KIAA0275 gene<br>product  | 10pter-<br>q25.3 |
| 361<br>65_<br>at | Cluster Incl. W51774:zc48b04.r1<br>Homo sapiens cDNA, 5 end<br>/clone=IMAGE-325519 /clone_end=5<br>/gb=W51774 /gi=1349666<br>/ug=Hs.74649 /len=678                   | COX6<br>C             | cytochrome c<br>oxidase subunit<br>VIc                            | 8q22-<br>q23     |

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| 361<br>_at       | Y13620 /FEATURE=<br>/DEFINITION=HSRNABCL9 Homo<br>sapiens mRNA for BCL9 gene   | BCL9         | B-cell<br>CLL/lymphoma<br>9                         | 1q21        |
| 362<br>39_<br>at | Cluster Incl. Z49194:H.sapiens mRNA<br>for oct-binding factor /cds=(523,1293)<br>/gb=Z49194 /gi=974830 /ug=Hs.2407<br>/len=3301                        | POU2<br>AF1  | POU domain,<br>class 2,<br>associating<br>factor 1  | 11q23.<br>1 |
| 364<br>64_<br>at | Cluster Incl. X94323:H.sapiens mRNA<br>for SGP28 protein /cds=(40,777)<br>/gb=X94323 /gi=1213612<br>/ug=Hs.54431 /len=2124                             | SGP28        | specific granule<br>protein (28 kDa)                | 6p12.3      |
| 365<br>36_<br>at | Cluster Incl. AF070614:Homo sapiens<br>clone 24732 unknown mRNA, partial<br>cds /cds=(0,1147) /gb=AF070614<br>/gi=3283878 /ug=Hs.61490 /len=1734       | SCHIP<br>1   | schwannomin-<br>interacting<br>protein 1            | 3q26.1      |
| 365<br>53_<br>at | Cluster Incl. AA669799:ag36c04.s1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-1118886 /clone_end=3<br>/gb=AA669799 /gi=2631298<br>/ug=Hs.6315 /len=679 | ASMT<br>L    | acetylserotonin<br>O-<br>methyltransfera<br>se-like | Xp22.3      |
| 365<br>71_<br>at | Cluster Incl. X68060:H.sapiens top1lb<br>mRNA for topoisomerase IIb<br>/cds=(0,4865) /gb=X68060 /gi=37230<br>/ug=Hs.75248 /len=4866                    | TOP2<br>B    | topoisomerase<br>(DNA) II beta<br>(180kD)           | 3p24        |
| 365<br>88_<br>at | Cluster Incl. AB018353:Homo sapiens<br>mRNA for KIAA0810 protein, partial<br>cds /cds=(0,2475) /gb=AB018353<br>/gi=3882340 /ug=Hs.7531 /len=4047       | KIAA0<br>810 | KIAA0810<br>protein                                 |             |

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| 366<br>01_<br>at   | Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102                            | VCL   | vinculin                                    | 10q22.1-q23 |
| 366<br>07_<br>at   | Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606               |       |   |             |
| 366<br>08_<br>at   | Cluster Incl. D55654:Human mRNA for cytosolic malate dehydrogenase, complete cds /cds=(55,1059) /gb=D55654 /gi=1255603 /ug=Hs.75375 /len=1267 | MDH1  | malate dehydrogenase 1, NAD (soluble)       | 2p16        |
| 366<br>29_<br>at   | Cluster Incl. A1635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295060 /clone_end=3 /gb=A1635895 /gi=4687225 /ug=Hs.75450 /len=1082  | DSIPI | delta sleep inducing peptide, immunoreactor | Xp21.1-q25  |
| 366<br>38_<br>at   | Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312          | CTGF  | connective tissue growth factor             | 6q23.1      |
| 366<br>44_<br>at   | Cluster Incl. D29963:Homo sapiens mRNA for CD151, complete cds /cds=(84,845) /gb=D29963 /gi=2073384 /ug=Hs.75564 /len=1486                    | CD151 | CD151 antigen                               | 11p15.5     |
| 366<br>61_<br>s_at | Cluster Incl. X06882:Human gene for CD14 differentiation antigen /cds=(105,1232) /gb=X06882 /gi=29736 /ug=Hs.75627 /len=1356                  | CD14  | CD14 antigen                                | 5q31.1      |

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|                  | /gi=29736 /ug=Hs.75627 /len=1356  |         |  |               |
| 366<br>67_<br>at | Cluster Incl. U47025:Human fetal brain glycogen phosphorylase B mRNA, complete cds /cds=(34,2565) /gb=U47025 /gi=1172225 /ug=Hs.75658 /len=4055 | PYGB    | "phosphorylase, glycogen; brain"                                       | 20p11.2-p11.1 |
| 366<br>90_<br>at | Cluster Incl. M10901:Human glucocorticoid receptor alpha mRNA, complete cds /cds=(132,2465) /gb=M10901 /gi=183032 /ug=Hs.75772 /len=4788        | NR3C1   | nuclear receptor subfamily 3, group C, member 1                        | 5q31          |
| 367<br>09_<br>at | Cluster Incl. Y00093:H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95 /cds=(64,3555) /gb=Y00093 /gi=35175 /ug=Hs.51077 /len=4654      | ITGAX   | integrin, alpha X (antigen CD11C (p150), alpha polypeptide)            | 16p11.2       |
| 367<br>10_<br>at | Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615                    | CAMP    | cathelicidin antimicrobial peptide                                     | 3p21.3        |
| 367<br>49_<br>at | Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633                 |         |  |               |
| 367<br>66_<br>at | Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735                    | RNAS E2 | ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) | 14q24-q31     |

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| 367<br>73_<br>f_at     | Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171                              | HLA-DQB1 | major histocompatibility complex, class II, DQ beta 1 | 6p21.3  |
| 367<br>90_<br>at       | Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633  | TPM1     | tropomyosin 1 (alpha)                                 | 15q22.1 |
| 367<br>98_<br>g_a<br>t | Cluster Incl. J04168:Human leukosialin mRNA, complete cds /cds=(95,1297) /gb=J04168 /gi=187118 /ug=Hs.80738 /len=2288   | SPN      | sialophorin (gpL115, leukosialin, CD43)               | 16p11.2 |
| 368<br>02_<br>at       | Cluster Incl. M23197:Human differentiation antigen (CD33) mRNA, complete cds /cds=(12,1106) /gb=M23197 /gi=180097 /ug=Hs.83731 /len=1437                                  | CD33     | CD33 antigen (gp67)                                   | 19q13.3 |
| 368<br>09_<br>at       | Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586 | CLC      | Charot-Leyden crystal protein                         | 19q13.1 |
| 368<br>43_<br>at       | Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein, complete cds /cds=(296,3424) /gb=AB005666 /gi=2389008 /ug=Hs.7019 /len=3885                       | SIPA1    | signal-induced proliferation-associated gene 1        | 11q13.3 |
| 368<br>73_             | Cluster Incl. D16532:Human gene for very low density lipoprotein receptor,  |          |   |         |

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| at                 | 5flanking and /cds=(615,3236)<br>/gb=D16532 /gi=407220 /ug=Hs.73729<br>/len=3853   |              |   |              |
| 368<br>78_<br>f_at | Cluster Incl. M60028:Human MHC<br>class II HLA-DQ-beta (DQB1,DQw9),<br>complete cds /cds=(57,842)<br>/gb=M60028 /gi=188114 /ug=Hs.73931<br>/len=1192   | HLA-<br>DQB1 | major<br>histocompatibilit<br>y complex, class<br>II, DQ beta 1 | 6p21.3       |
| 368<br>81_<br>at   | Cluster Incl. X71129:H.sapiens mRNA<br>for electron transfer flavoprotein beta<br>subunit /cds=(27,794) /gb=X71129<br>/gi=297901 /ug=Hs.74047 /len=835 | ETFB         | electron-<br>transfer-<br>flavoprotein,<br>beta polypeptide     | 19q13.<br>3  |
| 368<br>94_<br>at   | Cluster Incl. AL031846:dJ742C19.5<br>(novel Chromobox protein)<br>/cds=(89,844) /gb=AL031846<br>/gi=4164368 /ug=Hs.7442 /len=3964                      |              |   |              |
| 369<br>00_<br>at   | Cluster Incl. U52426:Homo sapiens<br>GOK (STIM1) mRNA, complete cds<br>/cds=(565,2622) /gb=U52426<br>/gi=2264345 /ug=Hs.74597 /len=4040.               | STIM1        | stromal<br>interaction<br>molecule 1                            | 11p15.<br>5  |
| 369<br>36_<br>at   | Cluster Incl. U58766:Human FX<br>protein mRNA, complete cds<br>/cds=(74,1039) /gb=U58766<br>/gi=1381178 /ug=Hs.75801 /len=1330                         | TSTA3        | tissue specific<br>transplantation<br>antigen P35B              | 8q24.3       |
| 369<br>45_<br>at   | Cluster Incl. X94910:Homo sapiens<br>mRNA for ERp28 protein<br>/cds=(11,796) /gb=X94910<br>/gi=3413292 /ug=Hs.75841 /len=892                           | C12orf<br>8  | chromosome 12<br>open reading<br>frame 8                        | 12q24.<br>13 |

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| 369<br>52_<br>at | Cluster Incl. D16480:Homo sapiens mRNA for mitochondrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein, complete cds /cds=(27,2318) /gb=D16480 /gi=493657 /ug=Hs.75860 /len=2690 | HADH<br>A | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit | 2p23                  |
| 369<br>63_<br>at | Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324 /ug=Hs.75888 /len=1536   | PGD       | phosphogluconate dehydrogenase  | 1p36.3<br>-<br>p36.13 |
| 369<br>73_<br>at | Cluster Incl. U41371:Human spliceosome associated protein (SAP 145) mRNA, complete cds /cds=(48,2666) /gb=U41371 /gi=1173904 /ug=Hs.75916 /len=2820   | SF3B2     | splicing factor 3b, subunit 2, 145kD  | 11q13.1               |
| 369<br>80_<br>at | Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,1096) /gb=U03105 /gi=476094 /ug=Hs.75969 /len=2061   | B4-2      | proline-rich protein with nuclear targeting signal  | 6q16.1                |
| 369<br>96_<br>at | Cluster Incl. U41635:Human OS-9 precursor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736   | OS-9      | amplified in osteosarcoma   | 12q13                 |
| 370<br>01_       | Homo sapiens /REF=M23254 /DEF=Cluster Incl. :Human Ca2-   | CAPN<br>2 | calpain 2, (m/II) large subunit   | 1q41-q42              |

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| at               | activated neutral protease large subunit (CANP) mRNA, complete cds /cds=(130,2232) /gb= /gi=511636 /ug=Hs.76288 /len=3213 /LEN=3435                       | 2           | large subunit                              | q42       |
| 370<br>15_<br>at | Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560                                       | ALDH1<br>A1 | aldehyde dehydrogenase 1 family, member A1 | 9q21      |
| 370<br>18_<br>at | Cluster Incl. A189287:qd05c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1722822 /clone_end=3 /gb=A189287 /gi=3740496 /ug=Hs.7644 /len=738                  | H1F2        | H1 histone family, member 2                | 6p21.3    |
| 370<br>21_<br>at | Cluster Incl. X16832:Human mRNA for cathepsin H (EC 3.4.22.16) /cds=(34,1041) /gb=X16832 /gi=29709 /ug=Hs.76476 /len=1399                                 | CTSH        | cathepsin H                                | 15q24-q25 |
| 370<br>23_<br>at | Cluster Incl. J02923:Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds /cds=(74,1957) /gb=J02923 /gi=189501 /ug=Hs.76506 /len=3175              | LCP1        | lymphocyte cytosolic protein 1 (L-plastin) | 13q14.3   |
| 370<br>26_<br>at | Cluster Incl. AF001461:Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA, complete cds /cds=(30,881) /gb=AF001461 /gi=3378030 /ug=Hs.76526 /len=1354 | COPE<br>B   | core promoter element binding protein      | 10p15     |
| 370<br>27_<br>at | Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899  | AHNA<br>K   | AHNAK nucleoprotein (desmoyokin)           | 11q12-q13 |



|                  |  |             |  |                  |
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| at               | /gi=178282 /ug=Hs.76549 /len=4051  |             | (desmoyokin)   |                  |
| 370<br>29_<br>at | Homo sapiens /REF=X83218<br>/DEF=Cluster Incl. :H.sapiens mRNA<br>for ATP synthase /cds=(36,677) /gb=<br>/gi=1008079 /ug=Hs.76572 /len=750<br>/LEN=826                           | ATP5<br>O   | ATP synthase,<br>H+ transporting,<br>mitochondrial<br>F1 complex, O<br>subunit<br>(oligomycin<br>sensitivity<br>conferring<br>protein) | 21q22.<br>11     |
| 370<br>39_<br>at | Cluster Incl. J00194:human hla-dr<br>antigen alpha-chain mrna & ivs<br>fragments /cds=(26,790) /gb=J00194<br>/gi=188231 /ug=Hs.76807 /len=1199                                   | HLA-<br>DRA | major<br>histocompatibilit<br>y complex, class<br>II, DR alpha   | 6p21.3           |
| 370<br>54_<br>at | Cluster Incl. J04739:Human<br>bactericidal permeability increasing<br>protein (BPI) mRNA, complete cds<br>/cds=(30,1493) /gb=J04739<br>/gi=179528 /ug=Hs.89535 /len=1813         | BPI         | bactericidal/per<br>meability-<br>increasing<br>protein  | 20q11.<br>23-q12 |
| 370<br>99_<br>at | Cluster Incl. AI806222:wf26e10.x1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-2356746 /clone_end=3<br>/gb=AI806222 /gi=5392788<br>/ug=Hs.100194 /len=563                         | ALOX5<br>AP | arachidonate 5-<br>lipoxygenase-<br>activating<br>protein  | 13q12            |
| 371<br>47_<br>at | Cluster Incl. AF020044:Homo sapiens<br>lymphocyte secreted C-type lectin<br>precursor, mRNA, complete cds<br>/cds=(179,1150) /gb=AF020044<br>/gi=2828595 /ug=Hs.105927 /len=1391 | SCGF        | "stem cell<br>growth factor;<br>lymphocyte<br>secreted C-type<br>lectin"   | 19q13.<br>3      |

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| 371<br>49_<br>s_at | Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607                                       |                |  |             |
| 371<br>59_<br>at   | Cluster Incl. U79259:Human clone 23945 mRNA, complete cds /cds=(636,1403) /gb=U79259 /gi=1710213 /ug=Hs.10700 /len=1683   | DJ159<br>A19.3 | hypothetical<br>protein  | 1p36.1<br>3 |
| 372<br>63_<br>at   | Cluster Incl. U55206:Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds /cds=(59,1015) /gb=U55206 /gi=2957143 /ug=Hs.78619 /len=1265  | GGH            | gamma-<br>glutamyl<br>hydrolase<br>(conjugase,<br>folylpolygamma<br>glutamyl<br>hydrolase) | 8q12.1      |
| 373<br>11_<br>at   | Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242  |                |  |             |
| 373<br>26_<br>at   | "Cluster Incl. U93305:Homo sapiens A4 differentiation-dependent protein (A4), triple LIM domain protein (LMO6), and synaptophysin (SYP) genes, complete cds; and calcium channel alpha-1 subunit (CACNA1F) gene, partial cds /cds=(75,533) /gb=U93305 /gi=270759" |                |  |             |
| 373<br>33_<br>at   | Cluster Incl. X63692:H.sapiens mRNA for DNA (cytosine-5)-methyltransferase /cds=(237,5087) /gb=X63692   | DNMT<br>1      | DNA (cytosine-<br>5-)-<br>methyltransfera  | 19p13.<br>2 |

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| at                 | /gi=1632818 /ug=Hs.77462 /len=5408  |          | se 1  |                 |
| 373<br>44_<br>at   | Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079                                       | HLA-DMA  | major histocompatibility complex, class II, DM alpha                                    | 6p21.3          |
| 373<br>84_<br>at   | Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(106,1470) /gb=D13640 /gi=286006 /ug=Hs.77961 /len=5134  | KIAA0015 | KIAA0015 gene product   | 22q11.22        |
| 373<br>99_<br>at   | Cluster Incl. D17793:Human mRNA for KIAA0119 gene, complete cds /cds=(51,1022) /gb=D17793 /gi=457407 /ug=Hs.78183 /len=1204   | AKR1C3   | aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) | 10p15-p14       |
| 374<br>03_<br>at   | Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /ug=Hs.78225 /len=1399   | ANXA1    | annexin A1  | 9q12-q21.2      |
| 374<br>07_<br>s_at | Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580 | MYH11    | myosin, heavy polypeptide 11, smooth muscle   | 16p13.13-p13.12 |
| 374<br>08_<br>at   | Cluster Incl. AB014609:Homo sapiens mRNA for KIAA0709 protein, complete cds /cds=(116,4555) /gb=AB014609 /gi=3327231 /ug=Hs.7835 /len=5641                                      | KIAA0709 | endocytic receptor (macrophage mannose receptor family)                                 | 17q24.1         |

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|                  |  |            | receptor family)                            |            |
| 374<br>17_<br>at | Cluster Incl. M36542:Human lymphoid-specific transcription factor mRNA, complete cds /cds=(54,1445) /gb=M36542 /gi=339495 /ug=Hs.1101 /len=2048  | POU2<br>F2 | POU domain, class 2, transcription factor 2 | 19q13.31   |
| 375<br>79_<br>at | Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881  | PIR12<br>1 | cytoplasmic FMRP interacting protein 2      | 5q34       |
| 376<br>00_<br>at | Cluster Incl. U68186:Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660683 /ug=Hs.81071 /len=1819   | ECM1       | extracellular matrix protein 1              | 1q21       |
| 376<br>15_<br>at | Cluster Incl. D86962:Human mRNA for KIAA0207 gene, complete cds /cds=(781,2547) /gb=D86962 /gi=1503997 /ug=Hs.81875 /len=5431  | GRB1<br>0  | growth factor receptor-bound protein 10     | 7p12-p11.2 |
| 376<br>25_<br>at | Cluster Incl. U52682:Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds /cds=(125,1477) /gb=U52682 /gi=1378108 /ug=Hs.82132 /len=5320 | IRF4       | interferon regulatory factor 4              | 6p25-p23   |
| 376<br>57_<br>at | Cluster Incl. Y16270:Homo sapiens PALM gene, exon 1 and joined CDS /cds=(145,1308) /gb=Y16270 /gi=3219601 /ug=Hs.78482 /len=2823   |            |   |            |

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| 376<br>69_<br>s_at | Cluster Incl. U16799:Human Na,K-ATPase beta-1 subunit mRNA, complete cds /cds=(45,950) /gb=U16799 /gi=806753 /ug=Hs.78629 /len=1476                   | ATP1B<br>1 | ATPase, Na+/K+ transporting, beta polypeptide 1 | 1q22-q25 |
| 377<br>01_<br>at   | Cluster Incl. L13463:Human helix-loop-helix basic phosphoprotein (G0S8) mRNA, complete cds /cds=(32,667) /gb=L13463 /gi=292054 /ug=Hs.78944 /len=1345 | RGS2       | regulator of G-protein signalling 2, 24kD       | 1q31     |
| 377<br>39_<br>at   | Cluster Incl. M86737:Human high mobility group box (SSRP1) mRNA, complete cds /cds=(274,2403) /gb=M86737 /gi=184241 /ug=Hs.79162 /len=2825            | SSRP<br>1  | structure specific recognition protein 1        | 11q12    |
| 377<br>47_<br>at   | Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gi=2182176 /ug=Hs.79274 /len=1597  |            |   |          |
| 377<br>55_<br>at   | Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete cds /cds=(359,1927) /gb=AB023169 /gi=4589547 /ug=Hs.7935 /len=4856            | KIAA0952   | KIAA0952 protein                                | 20p12.1  |
| 377<br>62_<br>at   | Cluster Incl. Y07909:H.sapiens mRNA for Progression Associated Protein 1 /cds=(218,691) /gb=Y07909 /gi=1542882 /ug=Hs.79368 /len=2774                 | EMP1       | epithelial membrane protein 1                   | 12p12.3  |
| 377<br>75_         | Cluster Incl. W25951:17d10 Homo sapiens cDNA /gb=W25951   |            | septin 6  | Xq24     |

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| at                 | /gi=1306236 /ug=Hs.123282 /len=738   |              |   |              |
| 378<br>09_<br>at   | Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411                                    | HOXA<br>9    | homeo box A9  | 7p15-<br>p14 |
| 378<br>11_<br>at   | Cluster Incl. AF042792:Homo sapiens alpha 2 delta calcium channel subunit isoform .1 mRNA, complete cds /cds=(161,3598) /gb=AF042792 /gi=2781438 /ug=Hs.127436 /len=5463 | CACN<br>A2D2 | calcium<br>channel,<br>voltage-<br>dependent,<br>alpha 2/delta<br>subunit 2 | 3p21.3       |
| 378<br>97_<br>s_at | Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493903 /clone_end=3 /gb=AI985964 /gi=5813241 /ug=Hs.82961 /len=487                              | TFF3         | trefoil factor 3<br>(intestinal)  | 21q22.<br>3  |
| 379<br>26_<br>at   | Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, complete cds /cds=(558,1217) /gb=D14520 /gi=303596 /ug=Hs.84728 /len=1301                              | KLF5         | Kruppel-like<br>factor 5<br>(intestinal)                                    | 13q21.<br>32 |
| 379<br>54_<br>at   | Cluster Incl. X16662:Human mRNA for vascular anticoagulant-beta (VAC-beta) /cds=(106,1089) /gb=X16662 /gi=37638 /ug=Hs.87268 /len=1940                                   | ANXA<br>8    | annexin A8  | 10q11.<br>2  |
| 379<br>67_<br>at   | Cluster Incl. AF000424:Homo sapiens LST1 mRNA, cLST1/C splice variant, complete cds /cds=(225,500) /gb=AF000424 /gi=2145063  | LY117        | lymphocyte<br>antigen 117   | 6p21.3       |

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|--------------------|---|--------------|---|----------------|
|                    | /ug=Hs.88411 /len=635   |              |   |                |
| 379<br>92_<br>s_at | Cluster Incl. AI436567:ti03b09.x1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-2129369 /clone_end=3<br>/gb=AI436567 /gi=4282731<br>/ug=Hs.89761 /len=680                       | ATP5D        | ATP synthase,<br>H <sup>+</sup> transporting,<br>mitochondrial<br>F1 complex,<br>delta subunit            | 19p13.<br>3    |
| 380<br>06_<br>at   | Cluster Incl. M37766:Human MEM-102<br>glycoprotein mRNA, complete cds<br>/cds=(20,751) /gb=M37766 /gi=187518<br>/ug=Hs.901 /len=1058  | CD48         | CD48 antigen<br>(B-cell<br>membrane<br>protein)   | 1q21.3<br>-q22 |
| 380<br>17_<br>at   | Cluster Incl. U05259:Human MB-1<br>gene, complete cds /cds=(36,716)<br>/gb=U05259 /gi=452561 /ug=Hs.79630<br>/len=1107  |              |   |                |
| 380<br>37_<br>at   | Cluster Incl. M60278:Human heparin-<br>binding EGF-like growth factor mRNA,<br>complete cds /cds=(261,887)<br>/gb=M60278 /gi=183866 /ug=Hs.799<br>/len=2342                   | DTR          | diphtheria toxin<br>receptor<br>(heparin-binding<br>epidermal<br>growth factor-<br>like growth<br>factor) | 5q23           |
| 380<br>63_<br>at   | Cluster Incl. U00952:Human clone<br>A9A2BRB7 (CAC) <sub>n</sub> /(GTG) <sub>n</sub> repeat-<br>containing mRNA /cds=UNKNOWN<br>/gb=U00952 /gi=405054 /ug=Hs.8068<br>/len=1047 |              |   |                |
| 380<br>95_<br>_at  | Cluster Incl. M83664:Human MHC<br>class II lymphocyte antigen (HLA-DP)<br>beta chain mRNA, complete cds<br>/cds=(59,835) /gb=M83664 /gi=188478                                | HLA-<br>DPB1 | major<br>histocompatibilit<br>y complex, class<br>II, DP beta 1   | 6p21.3         |

|                        |  |          |  |          |
|------------------------|--|----------|--|----------|
|                        | /ug=Hs.814 /len=1501   |          | II, DP beta 1  |          |
| 380<br>96_<br>f_at     | Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501                                 | HLA-DPB1 | major histocompatibility complex, class II, DP beta 1                  | 6p21.3   |
| 380<br>97_<br>at       | Cluster Incl. AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165   | PIG8     | etoposide-induced mRNA   | 11q24    |
| 381<br>12_<br>g_a<br>t | "Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224" | CSPG 2   | chondroitin sulfate proteoglycan 2 (versican)                          | 5q14.3   |
| 381<br>16_<br>at       | Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836  | KIAA0101 | KIAA0101 gene product  | 15q22.1  |
| 381<br>47_<br>at       | Cluster Incl. AL023657:Homo sapiens SH2D1A cDNA, formerly known as DSHP /cds=(299,685) /gb=AL023657 /gi=3153107 /ug=Hs.151544 /len=2530  | SH2D1A   | SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) | Xq25-q26 |
| 381<br>94_<br>s_at     | Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds /cds=(0,1049) /gb=M63438 /gi=184847   | IGKC     | immunoglobulin kappa constant  | 2p12     |



|                  |   |              |   |              |
|------------------|---|--------------|---|--------------|
|                  | /ug=Hs.156110 /len=1244   |              |   |              |
| 382<br>25_<br>at | Cluster Incl. AF052728:Homo sapiens<br>HERG-USO (HERG) mRNA,<br>alternatively spliced, partial cds<br>/cds=(0,284) /gb=AF052728<br>/gi=3549258 /ug=Hs.165664 /len=767 | KCNH<br>2    | potassium<br>voltage-gated<br>channel,<br>subfamily H<br>(eag-related),<br>member 2 | 7q35-<br>q36 |
| 382<br>33_<br>at | Cluster Incl. AF093265:Homo sapiens<br>homer-3 mRNA, complete cds<br>/cds=(90,1166) /gb=AF093265<br>/gi=3834620 /ug=Hs.166146 /len=1407                               | HOME<br>R-3  | Homer,<br>neuronal<br>immediate early<br>gene, 3                                    | 19p13.<br>12 |
| 382<br>69_<br>at | "Cluster Incl. AL050147:Homo sapiens<br>mRNA; cDNA DKFZp586E0820 (from<br>clone DKFZp586E0820) /cds=(0,1630)<br>/gb=AL050147 /gi=4884153<br>/ug=Hs.91146 /len=1837"   | PKD2         | protein kinase<br>D2  | 19q13.<br>2  |
| 383<br>12_<br>at | "Cluster Incl. AL050002:Homo sapiens<br>mRNA; cDNA DKFZp564O222 (from<br>clone DKFZp564O222)<br>/cds=UNKNOWN /gb=AL050002<br>/gi=4884256 /ug=Hs.94795 /len=1546"      |              |   |              |
| 383<br>19_<br>at | Cluster Incl. AA919102:ol84h02.s1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-1536339 /clone_end=3<br>/gb=AA919102 /gi=3058992<br>/ug=Hs.95327 /len=622               | CD3D         | CD3D antigen,<br>delta<br>polypeptide<br>(TIT3 complex)                             | 11q23        |
| 383<br>36_<br>at | Cluster Incl. AB023230:Homo sapiens<br>mRNA for KIAA1013 protein, partial<br>cds /cds=(0,3188) /gb=AB023230<br>/gi=4589675 /ug=Hs.96427 /len=4783                     | KIAA1<br>013 | KIAA1013<br>protein   | 3            |

|                        |   |             |  |              |
|------------------------|---|-------------|--|--------------|
|                        | /gi=4589675 /ug=Hs.96427 /len=4783  |             |  |              |
| 383<br>61_<br>g_a<br>t | Cluster Incl. AI688812:wd41c03.x1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-2330692 /clone_end=3<br>/gb=AI688812 /gi=4900106<br>/ug=Hs.99491 /len=504           | RASG<br>RP2 | RAS guanyl<br>releasing<br>protein 2<br>(calcium and<br>DAG-regulated) | 11q13        |
| 383<br>91_<br>at       | Cluster Incl. M94345:Homo sapiens<br>macrophage capping protein mRNA,<br>complete cds /cds=(49,1095)<br>/gb=M94345 /gi=187455 /ug=Hs.82422<br>/len=1221           | CAPG        | capping protein<br>(actin filament),<br>gelsolin-like                  | 2cen-<br>q24 |
| 384<br>14_<br>at       | Cluster Incl. U05340:Human p55CDC<br>mRNA, complete cds /cds=(110,1609)<br>/gb=U05340 /gi=468031 /ug=Hs.82906<br>/len=1686  | CDC2<br>0   | CDC20 (cell<br>division cycle<br>20, S.<br>cerevisiae,<br>homolog)     | 9q13-<br>q21 |
| 384<br>15_<br>at       | Cluster Incl. U14603:Human protein-<br>tyrosine phosphatase (HU-PP-1)<br>mRNA, partial sequence<br>/cds=(423,926) /gb=U14603<br>/gi=894158 /ug=Hs.82911 /len=1526 | PTP4A<br>2  | protein tyrosine<br>phosphatase<br>type IVA,<br>member 2               | 1p35         |
| 384<br>35_<br>at       | Cluster Incl. U25182:Human<br>antioxidant enzyme AOE37-2 mRNA,<br>complete cds /cds=(43,858)<br>/gb=U25182 /gi=799380 /ug=Hs.83383<br>/len=921                    | PRDX<br>4   | peroxiredoxin 4  | Xp22.1<br>3  |
| 384<br>65_<br>at       | Cluster Incl. M37721:Human<br>peptidylglycine alpha-amidating<br>monooxygenase mRNA, complete cds<br>/cds=(188,3112) /gb=M37721                                   | PAM         | peptidylglycine<br>alpha-amidating<br>monooxygenase                    | 5q14-<br>q21 |

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|                  | /gi=189594 /ug=Hs.83920 /len=3748  |          |  |                  |
| 384<br>72_<br>at | Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0,2658) /gb=D63477 /gi=1469867 /ug=Hs.84087 /len=5286                         | KIAA0143 | KIAA0143 protein   | 8q24.2<br>2      |
| 384<br>85_<br>at | Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549 /len=553                            | NDUF C1  | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI) | 4q28.2<br>-q31.1 |
| 384<br>87_<br>at | Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777                         |          |  |                  |
| 385<br>77_<br>at | Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429                 |          |  |                  |
| 385<br>78_<br>at | Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204 | TNFR SF7 | tumor necrosis factor receptor superfamily, member 7                 | 12p13            |
| 386<br>53_<br>at | Cluster Incl. D11428:Homo sapiens mRNA for PMP-22(PAS-II/SR13/Gas-3), complete cds /cds=(188,670) /gb=D11428 /gi=220009 /ug=Hs.103724 /len=1806    | PMP22    | peripheral myelin protein 22   | 17p12-<br>p11.2  |

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| 386<br>66_<br>at | Cluster Incl. M85169:Human<br>homologue of yeast sec7 mRNA,<br>complete cds /cds=(69,1265)<br>/gb=M85169 /gi=338001 /ug=Hs.1050<br>/len=3301                       | PSCD<br>1    | pleckstrin<br>homology, Sec7<br>and coiled/coil<br>domains<br>1(cytohesin 1)                          | 17q25            |
| 386<br>95_<br>at | Cluster Incl. AA203303:zx55b01.r1<br>Homo sapiens cDNA, 5 end<br>/clone=IMAGE-446377 /clone_end=5<br>/gb=AA203303 /gi=1799194<br>/ug=Hs.10758 /len=876             | NDUF<br>S4   | NADH<br>dehydrogenase<br>(ubiquinone) Fe-<br>S protein 4<br>(18kD) (NADH-<br>coenzyme Q<br>reductase) | 5q11.1 *         |
| 387<br>05_<br>at | Cluster Incl. AI310002:qo77c11.x1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-1914548 /clone_end=3<br>/gb=AI310002 /gi=4004873<br>/ug=Hs.108332 /len=656           | UBE2<br>D2   | ubiquitin-<br>conjugating<br>enzyme E2D 2<br>(homologous to<br>yeast UBC4/5)                          | 5p14.2<br>-q23.3 |
| 387<br>28_<br>at | Cluster Incl. D86978:Human mRNA for<br>KIAA0225 gene, partial cds<br>/cds=(0,6043) /gb=D86978<br>/gi=1504029 /ug=Hs.84790 /len=6237                                | KIAA0<br>225 | KIAA0225<br>protein   | 7q33             |
| 387<br>30_<br>at | Homo sapiens /REF=AB020671<br>/DEF=Cluster Incl. : mRNA for<br>KIAA0864 protein, partial cds<br>/cds=(0,3656) /gb= /gi=4240216<br>/ug=Hs.84883 /len=4319 /LEN=4481 | KIAA0<br>864 | KIAA0864<br>protein   | 17p11.<br>2      |
| 387<br>35_<br>at | Cluster Incl. AB011085:Homo sapiens<br>mRNA for KIAA0513 protein, complete<br>cds /cds=(631,1866) /gb=AB011085<br>/gi=3043549 /ug=Hs.85053 /len=7758               | KIAA0<br>513 | KIAA0513 gene<br>product  | 16q24.<br>1      |

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| 387<br>47_<br>at | Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616  |            |   |          |
| 387<br>67_<br>at | Cluster Incl. AF041037:Homo sapiens novel antagonist of FGF signaling (sprouty-1) mRNA, partial cds /cds=(0,419) /gb=AF041037 /gi=2827283 /ug=Hs.88044 /len=1586 | SPRY<br>1  | sprouty (Drosophila) homolog 1 (antagonist of FGF signaling)  | 4        |
| 387<br>80_<br>at | Cluster Incl. J04794:Human aldehyde reductase mRNA, complete cds /cds=(60,1037) /gb=J04794 /gi=178480 /ug=Hs.89529 /len=1132                                     | AKR1<br>A1 | aldo-keto reductase family 1, member A1 (aldehyde reductase)  | 1p33-p32 |
| 387<br>91_<br>at | Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936 /ug=Hs.89674 /len=1668                                     | DDOS<br>T  | dolichyl-diphosphooligosaccharide-protein glycosyltransferase | 1p36.1   |
| 388<br>08_<br>at | Cluster Incl. D64154:Human mRNA for Mr 110,000 antigen, complete cds /cds=(46,1269) /gb=D64154 /gi=994759 /ug=Hs.90107 /len=1375                                 | GP110      | cell membrane glycoprotein, 110000M(r) (surface antigen)      | 20q13.33 |
| 388<br>12_<br>at | Cluster Incl. X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5561) /gb=X79683 /gi=663206 /ug=Hs.90291 /len=5673   | LAMB<br>2  | laminin, beta 2 (laminin S)                                   | 3p21     |
| 388              | Cluster Incl. AF039103:Homo sapiens  | HTATI      | HIV-1 Tat   | 11p15.   |

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| 24_<br>at         | Tat-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297   | P2       | interactive protein 2, 30 kDa  | 1        |
| 388<br>33_<br>at  | Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048   | HLA-DPA1 | major histocompatibility complex, class II, DP alpha 1               | 6p21.3   |
| 388<br>58_<br>at  | Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) mRNA, complete cds /cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.188021 /len=4070   | KCNH2    | potassium voltage-gated channel, subfamily H (eag-related), member 2 | 7q35-q36 |
| 388<br>79_<br>at  | Cluster Incl. D83664:Human mRNA for CAAF1 (calcium-binding protein in amniotic fluid 1), complete cds /cds=(68,346) /gb=D83664 /gi=1502286 /ug=Hs.19413 /len=466   | S100A12  | S100 'calcium-binding protein A12 (calgranulin C)                    | 1q21     |
| 388<br>93_<br>at  | Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136 |          |  |          |
| 388<br>94_<br>g_a | Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains   |          |  |          |

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|--------------------|---|------------|--|-----------------|
| t                  | genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136 |            |  |                 |
| 388<br>95_i<br>_at | Cluster Incl. X77094:H.sapiens mRNA for p40phox /cds=(130,1149) /gb=X77094 /gi=458543 /ug=Hs.196352 /len=1245   | NCF4       | neutrophil cytosolic factor 4 (40kD)               | 22q13.1         |
| 389<br>17_<br>at   | Cluster Incl. X73617:H.sapiens mRNA for T-cell receptor delta /cds=UNKNOWN /gb=X73617 /gi=402624 /ug=Hs.2014 /len=2343  |            |  |                 |
| 389<br>49_<br>at   | Cluster Incl. L01087:Human protein kinase C-theta (PRKCT) mRNA, complete cds /cds=(94,2214) /gb=L01087 /gi=558098 /ug=Hs.211593 /len=2754                         | PRKC<br>Q  | protein kinase C, theta                            | 10p15           |
| 389<br>63_i<br>_at | Cluster Incl. U12707:Human Wiskott-Aldrich syndrome protein (WASP) mRNA, complete cds /cds=(34,1542) /gb=U12707 /gi=695150 /ug=Hs.2157 /len=1806                  | WAS        | Wiskott-Aldrich syndrome (eczema-thrombocytopenia) | Xp11.4 - p11.21 |
| 389<br>92_<br>at   | Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502 /ug=Hs.110713 /len=2699   | DEK        | DEK oncogene (DNA binding)                         | 6p23            |
| 389<br>94_<br>at   | Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913)   | STAT1<br>2 | STAT induced STAT inhibitor-2                      | 12q             |

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| at               | /gb=AF037989 /gi=3265032<br>/ug=Hs.110776 /len=1937   |            |   |                |
| 390<br>61_<br>at | Cluster Incl. D28137:Human mRNA for<br>BST-2, complete cds /cds=(9,551)<br>/gb=D28137 /gi=457563<br>/ug=Hs.118110 /len=996  | BST2       | bone marrow<br>stromal cell<br>antigen 2                              | 19p13.<br>2    |
| 390<br>62_<br>at | Cluster Incl. AL008726:dJ337O18.2<br>(Lysosomal Protective Protein<br>precursor (EC 3.4.16.5, Cathepsin A,<br>Carboxypeptidase C)) /cds=(133,1575)<br>/gb=AL008726 /gi=3183870<br>/ug=Hs.118126 /len=1946 |            |   |                |
| 390<br>70_<br>at | Cluster Incl. U03057:Human actin<br>bundling protein (HSN) mRNA,<br>complete cds /cds=(111,1592)<br>/gb=U03057 /gi=458027<br>/ug=Hs.118400 /len=2767  | SNL        | singed<br>(Drosophila)-like<br>(sea urchin<br>fascin homolog<br>like) | 7p22           |
| 390<br>89_<br>at | Cluster Incl. Y07604:H.sapiens mRNA<br>for nucleoside-diphosphate kinase<br>/cds=(11,574) /gb=Y07604<br>/gi=1945761 /ug=Hs.9235 /len=879  | NME4       | non-metastatic<br>cells 4, protein<br>expressed in                    | 16p13.<br>3    |
| 391<br>18_<br>at | Cluster Incl. L08069:Human heat<br>shock protein, E. coli DnaJ homologue<br>mRNA, complete cds /cds=(82,1275)<br>/gb=L08069 /gi=306713 /ug=Hs.94<br>/len=1438   | DNAJ<br>A1 | DnaJ (Hsp40)<br>homolog,<br>subfamily A,<br>member 1                  | 9p13-<br>p12   |
| 391<br>36_<br>at | Cluster Incl. AB017642:Homo sapiens<br>mRNA for oxidative-stress responsive<br>1, complete cds /cds=(342,1925)<br>/gb=AB017642 /gi=4519628  | OSR1       | oxidative-stress<br>responsive 1                                      | 3p22-<br>p21.3 |



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|------------------|--|--------------|---|---------------|
|                  | /ug=Hs.95220 /len=4519   |              |   |               |
| 391<br>65_<br>at | Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819                        | NIFU         | nitrogen fixation cluster-like  | 12q24.1       |
| 391<br>70_<br>at | "Cluster Incl. AL049957:Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323) /cds=UNKNOWN /gb=AL049957 /gi=4884209 /ug=Hs.99766 /len=2180" |              |   |               |
| 391<br>79_<br>at | Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637            | PRG2         | proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein) | 11q12         |
| 392<br>62_<br>at | Cluster Incl. U79266:Human clone 23627 mRNA, complete cds /cds=(184,1041) /gb=U79266 /gi=1710225 /ug=Hs.23642 /len=1561                                | HSU79<br>266 | protein predicted by clone 23627  | 11q13.1       |
| 393<br>01_<br>at | Cluster Incl. X85030:H.sapiens mRNA for skeletal muscle-specific calpain /cds=(0,2465) /gb=X85030 /gi=791039 /ug=Hs.239689 /len=2466                   | CAPN<br>3    | calpain 3, (p94)  | 15q15.1-q21.1 |
| 393<br>27_<br>at | Cluster Incl. D86983:Human mRNA for KIAA0230 gene, partial cds /cds=(0,4490) /gb=D86983 /gi=1504039 /ug=Hs.118893 /len=5510                            | D2S44<br>8   | Melanoma associated gene  | 2pter-p25.1   |

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| 393<br>58_<br>at | Cluster Incl. U37146:Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds /cds=(495,4982) /gb=U37146 /gi=1045654 /ug=Hs.120980 /len=5970 |             |   |                  |
| 396<br>10_<br>at | Cluster Incl. X16665:Human HOXB2 mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520   | HOXB<br>2   | homeo box B2  | 17q21-<br>q22    |
| 396<br>49_<br>at | Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236   | ARHG<br>AP4 | Rho GTPase<br>activating<br>protein 4   | Xq28             |
| 396<br>70_<br>at | "Cluster Incl. AL050034:Homo sapiens mRNA; cDNA DKFZp566G0224 (from clone DKFZp566G0224) /cds=(0,1380) /gb=AL050034 /gi=4884274 /ug=Hs.33573 /len=1762"                       | ADPR<br>TL3 | "ADP-<br>ribosyltransferase (NAD+; poly<br>(ADP-ribose)<br>polymerase)-like<br>3" | 3p22.2<br>-p21.1 |
| 396<br>89_<br>at | Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778                                  | CST3        | cystatin C<br>(amyloid<br>angiopathy and<br>cerebral<br>hemorrhage)               | 20p11.<br>2      |
| 397<br>30_<br>at | Cluster Incl. X16416:Human c-abl mRNA encoding p150 protein /cds=(147,3539) /gb=X16416 /gi=28236 /ug=Hs.146355 /len=5527  | ABL1        | v-abl Abelson<br>murine leukemia<br>viral oncogene<br>homolog 1                   | 9q34.1           |
| 397<br>55_<br>at | Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on  |             |   |                  |

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| at                     | chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802  |              |  |             |
| 397<br>56_<br>g_a<br>t | Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802 |              |  |             |
| 397<br>75_<br>at       | Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827  |              |  |             |
| 398<br>01_<br>at       | Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735   | PLOD<br>3    | procollagen-<br>lysine, 2-<br>oxoglutarate 5-<br>dioxygenase 3 | 7q22        |
| 398<br>14_<br>s_at     | Cluster Incl. AI052724:oz27a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676542 /clone_end=3 /gb=AI052724 /gi=3308715 /ug=Hs.109201 /len=682  | LOC51<br>635 | CGI-86 protein   | 14q23.<br>1 |
| 398<br>24_<br>at       | Cluster Incl. AI391564:tg16b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108907 /clone_end=3  |              | ESTs, Weakly<br>similar to<br>A28996 proline-                  |             |

|                  |   |              |   |                   |
|------------------|---|--------------|---|-------------------|
| at               | /gb=AI391564 /gi=4217568<br>/ug=Hs.110820 /len=442  |              | rich protein M14<br>precursor<br>mouse<br>[M.musculus]                                  |                   |
| 398<br>27_<br>at | Cluster Incl. AA522530:ni38d12.s1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-979127 /clone_end=3<br>/gb=AA522530 /gi=2263242<br>/ug=Hs.111244 /len=891 | FLJ20<br>500 | hypothetical<br>protein   | 10pter-<br>q26.12 |
| 398<br>60_<br>at | Cluster Incl. U05040:Human FUSE<br>binding protein mRNA, complete cds<br>/cds=(26,1960) /gb=U05040<br>/gi=460151 /ug=Hs.118962 /len=2325                |              | Homo sapiens<br>far upstream<br>element (FUSE)<br>binding protein<br>1 (FUBP1),<br>mRNA |                   |
| 399<br>21_<br>at | Cluster Incl. AI526089:DU3.2-7.H07.r<br>Homo sapiens cDNA, 5 end<br>/clone_end=5 /gb=AI526089<br>/gi=4440207 /ug=Hs.1342 /len=788                       | COX5<br>B    | cytochrome c<br>oxidase subunit<br>Vb   | 2cen-<br>q13      |
| 399<br>29_<br>at | Cluster Incl. AB023139:Homo sapiens<br>mRNA for KIAA0922 protein, partial<br>cds /cds=(0,2372) /gb=AB023139<br>/gi=4589475 /ug=Hs.37892 /len=2505       | KIAA0<br>922 | KIAA0922<br>protein   | 4q31.3            |
| 399<br>68_<br>at | Cluster Incl. U50136:Human<br>leukotriene C4 synthase (LTC4S)<br>gene, complete cds /cds=(96,548)<br>/gb=U50136 /gi=1314482 /ug=Hs.456<br>/len=665      |              |   |                   |
| 399<br>93_<br>at | Cluster Incl. D11466:Homo sapiens<br>mRNA for PIG-A protein, complete cds   | PIGA         | phosphatidylinositol<br>glycan,   | Xp22.1            |

|                    |  |           |   |                 |
|--------------------|--|-----------|---|-----------------|
| at                 | /cds=(85,1539) /gb=D11466<br>/gi=219993 /ug=Hs.51 /len=3589  |           | class A<br>(paroxysmal<br>nocturnal<br>hemoglobinuria)  |                 |
| 400<br>81_<br>at   | Cluster Incl. L26232:Human<br>phospholipid transfer protein mRNA,<br>complete cds /cds=(87,1568)<br>/gb=L26232 /gi=468325<br>/ug=Hs.154854 /len=1750                       | PLTP      | phospholipid<br>transfer protein  | 20q12-<br>q13.1 |
| 401<br>59_<br>r_at | Cluster Incl. M55067:Human 47-kD<br>autosomal chronic granulomatous<br>disease protein mRNA, complete cds<br>/cds=(22,1194) /gb=M55067<br>/gi=189050 /ug=Hs.1583 /len=1349 | NCF1      | neutrophil<br>cytosolic factor<br>1 (47kD, chronic<br>granulomatous<br>disease,<br>autosomal 1) | 7q11.2<br>3     |
| 401<br>98_<br>at   | Cluster Incl. L06132:Human voltage-<br>dependent anion channel isoform 1<br>(VDAC) mRNA, complete cds<br>/cds=(99,950) /gb=L06132 /gi=340198<br>/ug=Hs.149155 /len=1806    | VDAC<br>1 | voltage-<br>dependent<br>anion channel 1  | 5q31            |
| 402<br>81_<br>at   | Cluster Incl. D63878:Human mRNA for<br>KIAA0158 gene, complete cds<br>/cds=(258,1343) /gb=D63878<br>/gi=961447 /ug=Hs.155595 /len=3433                                     | NEDD<br>5 | neural precursor<br>cell expressed,<br>developmentally<br>down-regulated<br>5                   | 2q37            |
| 402<br>82_<br>s_at | Cluster Incl. M84526:Human<br>adipsin/complement factor D mRNA,<br>complete cds /cds=(54,740)<br>/gb=M84526 /gi=178625<br>/ug=Hs.155597 /len=1071                          | DF        | D component of<br>complement<br>(adipsin)   | 19p13.<br>3     |

|                  |   |        |  |               |
|------------------|---|--------|--|---------------|
| 403<br>96_<br>at | Cluster Incl. U49395:Human ionotropic ATP receptor P2X5a mRNA, complete cds /cds=(52,1317) /gb=U49395 /gi=1552521 /ug=Hs.77807 /len=1956                      | P2RX5  | purinergic receptor P2X, ligand-gated ion channel, 5                     | 17p13         |
| 404<br>07_<br>at | Cluster Incl. U28386:Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds /cds=(132,1721) /gb=U28386 /gi=899538 /ug=Hs.159557 /len=1976 | KPNA 2 | karyopherin alpha 2 (RAG cohort 1, importin alpha 1)                     | 17q23.1-q23.3 |
| 404<br>19_<br>at | Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035   |        |  |               |
| 404<br>56_<br>at | "Cluster Incl. AL049963:Homo sapiens mRNA; cDNA DKFZp564A132 (from clone DKFZp564A132) /cds=UNKNOWN /gb=AL049963 /gi=4884213 /ug=Hs.16726 /len=1322"          |        |  |               |
| 404<br>93_<br>at | Cluster Incl. L05424:Human hyaluronate receptor (CD44) gene /cds=(136,2211) /gb=L05424 /gi=950415 /ug=Hs.169610 /len=2905                                     |        |  |               |
| 405<br>09_<br>at | Cluster Incl. J04058:Human electron transfer flavoprotein alpha-subunit mRNA, complete cds /cds=(0,1001) /gb=J04058 /gi=182250 /ug=Hs.169919 /len=1266        | ETFA   | electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) | 15q23-q25     |
| 405              | Cluster Incl. D25538:Human mRNA for   | ADCY   | adenylate  | 16q12-        |

|                  |  |             |   |               |
|------------------|--|-------------|---|---------------|
| 85_<br>at        | KIAA0037 gene, complete cds<br>/cds=(265,3507) /gb=D25538<br>/gi=436217 /ug=Hs.172199 /len=6196  | 7           | cyclase 7   | q13           |
| 406<br>10_<br>at | Cluster Incl. AI743507:wf72a06.x2<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-2361106 /clone_end=3<br>/gb=AI743507 /gi=5111795<br>/ug=Hs.173518 /len=733     | ZFR         | zinc finger RNA<br>binding protein  | 5p13.3        |
| 406<br>98_<br>at | Cluster Incl. X96719:H.sapiens mRNA<br>for AICL (activation-induced C-type<br>lectin) /cds=(132,581) /gb=X96719<br>/gi=1632815 /ug=Hs.85201 /len=739         | CLEC<br>SF2 | C-type (calcium<br>dependent,<br>carbohydrate-<br>recognition<br>domain) lectin,<br>superfamily<br>member 2<br>(activation-<br>induced) | 12p13-<br>p12 |
| 407<br>18_<br>at | Cluster Incl. AF013611:Homo sapiens<br>lymphopain mRNA, complete cds<br>/cds=(0,1130) /gb=AF013611<br>/gi=2582044 /ug=Hs.87450 /len=1131                     | CTSW        | cathepsin W<br>(lymphopain)   | 11q13.<br>1   |
| 407<br>23_<br>at | Cluster Incl. AJ010059:Homo sapiens<br>SIT protein /cds=(87,677)<br>/gb=AJ010059 /gi=4688891<br>/ug=Hs.88012 /len=1232                                       | SIT         | SHP2<br>interacting<br>transmembrane<br>adaptor   | 9p13-<br>p12  |
| 407<br>63_<br>at | Cluster Incl. U85707:Human<br>leukemogenic homolog protein<br>(MEIS1) mRNA, complete cds<br>/cds=(65,1237) /gb=U85707<br>/gi=2058550 /ug=Hs.170177 /len=2511 | MEIS1       | Meis1 (mouse)<br>homolog  | 2p14-<br>p13  |

|                  |  |             |  |               |
|------------------|--|-------------|--|---------------|
| 407<br>67_<br>at | Cluster Incl. M59499:Human lipoprotein-associated coagulation inhibitor (LACI) gene /cds=(2,916) /gb=M59499 /gi=187205 /ug=Hs.170279 /len=3599   |             |  |               |
| 407<br>75_<br>at | Cluster Incl. AL021786:Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs /cds=(0,680) /gb=AL021786 /gi=2853186 /ug=Hs.17109 /len=1389 |             |  |               |
| 407<br>86_<br>at | Cluster Incl. U37352:Human protein phosphatase 2A Balphal regulatory subunit mRNA, complete cds /cds=(88,1632) /gb=U37352 /gi=1203811 /ug=Hs.171734 /len=4064  | PPP2<br>R5C | protein phosphatase 2, regulatory subunit B (B56), gamma isoform | 3p21          |
| 408<br>17_<br>at | Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650  | NUCB<br>1   | nucleobindin 1   | 19q13.2-q13.4 |
| 408<br>56_<br>at | Cluster Incl. U29953:Human pigment epithelium-derived factor gene, complete cds /cds=(136,1224) /gb=U29953 /gi=1144298 /ug=Hs.173594 /len=1511   |             |  |               |
| 408<br>64_<br>at | Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D25274 /gi=464185 /ug=Hs.173737 /len=1232  |             |  |               |



|                    |  |         |   |         |
|--------------------|--|---------|---|---------|
|                    | /gi=464185 /ug=Hs.173737 /len=1232   |         |   |         |
| 408<br>65_<br>at   | Cluster Incl. U51166:Human G/T mismatch-specific thymine DNA glycosylase mRNA, complete cds /cds=(399,1631) /gb=U51166 /gi=1378106 /ug=Hs.173824 /len=3410 | TDG     | thymine-DNA glycosylase                                       | 12q24.1 |
| 409<br>36_<br>at   | Cluster Incl. AI651806:wb55f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2309611 /clone_end=3 /gb=AI651806 /gi=4735797 /ug=Hs.19280 /len=609                | CRIM1   | cysteine-rich motor neuron 1                                  | 2p21    |
| 410<br>96_<br>at   | Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446               | S100A8  | S100 calcium-binding protein A8 (calgranulin A)               | 1q21    |
| 411<br>38_<br>at   | Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M16279 /gi=188542 /ug=Hs.177543 /len=1238  | MIC2    | antigen identified by monoclonal antibodies 12E7, F21 and O13 | Xp22.32 |
| 411<br>53_<br>f_at | Cluster Incl. AF102803:untitled /cds=(2,2722) /gb=AF102803 /gi=4092760 /ug=Hs.178452 /len=3668   |         |   |         |
| 411<br>55_<br>at   | Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4,2799) /gb=U03100 /gi=414981 /ug=Hs.178452 /len=3526                                | CTNN A1 | catenin (cadherin-associated protein), alpha 1 (102kD)        | 5q31    |

|                        |  |              |   |               |
|------------------------|--|--------------|---|---------------|
|                        |  |              | (102kD)   |               |
| 411<br>56_<br>g_a<br>t | Cluster Incl. U03100:Human<br>alpha2(E)-catenin mRNA, complete<br>cds /cds=(4,2799) /gb=U03100<br>/gi=414981 /ug=Hs.178452 /len=3526   | CTNN<br>A1   | catenin<br>(cadherin-<br>associated<br>protein), alpha 1<br>(102kD) | 5q31          |
| 411<br>63_<br>at       | Cluster Incl. AL109672:Homo sapiens<br>mRNA full length insert cDNA clone<br>EUROIMAGE 755868 /cds=(98,751)<br>/gb=AL109672 /gi=5689836<br>/ug=Hs.179516 /len=1378                 | P24B         | integral type I<br>protein  | 15q24-<br>q25 |
| 411<br>64_<br>at       | Cluster Incl. X67301:H.sapiens mRNA<br>for IgM heavy chain constant region<br>(Ab63) /cds=(0,1361) /gb=X67301<br>/gi=38407 /ug=Hs.179543 /len=1453                                 | IGHM         | immunoglobulin<br>heavy constant<br>mu                              | 14q32.<br>33  |
| 411<br>65_<br>g_a<br>t | Cluster Incl. X67301:H.sapiens mRNA<br>for IgM heavy chain constant region<br>(Ab63) /cds=(0,1361) /gb=X67301<br>/gi=38407 /ug=Hs.179543 /len=1453                                 | IGHM         | immunoglobulin<br>heavy constant<br>mu                              | 14q32.<br>33  |
| 411<br>66_<br>at       | Cluster Incl. X58529:Human<br>rearranged immunoglobulin mRNA for<br>mu heavy chain enhancer and<br>constant region /cds=UNKNOWN<br>/gb=X58529 /gi=33480 /ug=Hs.179543<br>/len=2325 |              |   |               |
| 411<br>77_<br>at       | Cluster Incl. AW024285:wt69d06.x1<br>Homo sapiens cDNA, 3 end<br>/clone=IMAGE-2512715 /clone_end=3<br>/gb=AW024285 /gi=5877815   | FLJ12<br>443 | hypothetical<br>protein<br>FLJ12443                                 | 5p15.3<br>3   |

|                  |  |          |   |           |
|------------------|--|----------|---|-----------|
|                  | /ug=Hs.179882 /len=550   |          |   |           |
| 411<br>91_<br>at | Cluster Incl. AB023209:Homo sapiens mRNA for KIAA0992 protein, partial cds /cds=(0,2318) /gb=AB023209 /gi=4589627 /ug=Hs.180347 /len=4347          | KIAA0992 | palladin  | 4q32.3    |
| 411<br>93_<br>at | Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390                  | DUSP6    | dual specificity phosphatase 6  | 12q22-q23 |
| 412<br>00_<br>at | Cluster Incl. Z22555:H.sapiens encoding CLA-1 mRNA /cds=(69,1598) /gb=Z22555 /gi=397606 /ug=Hs.180616 /len=2552                                    | CD36L1   | CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 | 12q24.31  |
| 412<br>20_<br>at | Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938       | MSF      | MLL septin-like fusion  | 17q25     |
| 412<br>73_<br>at | Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695 |          |   |           |
| 413<br>38_<br>at | Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523          |          |   |           |

|                  |   |              |   |              |
|------------------|---|--------------|---|--------------|
| 413<br>96_<br>at | Cluster Incl. AB006629:Homo sapiens mRNA for KIAA0291 gene, partial cds /cds=(0,2856) /gb=AB006629 /gi=2564329 /ug=Hs.104717 /len=4943                              | CYLN2        | cytoplasmic linker 2  | 7q11.2<br>3  |
| 414<br>70_<br>at | Cluster Incl. AF027208:Homo sapiens AC133 antigen mRNA, complete cds /cds=(37,2634) /gb=AF027208 /gi=2688948 /ug=Hs.112360 /len=3794                                | PROM<br>L1   | prominin (mouse)-like 1                                       | 4p15.3<br>3  |
| 414<br>71_<br>at | Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604                             | S100A<br>9   | S100 calcium-binding protein A9 (calgranulin B)               | 1q21         |
| 415<br>03_<br>at | Cluster Incl. AB020661:Homo sapiens mRNA for KIAA0854 protein, complete cds /cds=(304,2817) /gb=AB020661 /gi=4240196 /ug=Hs.30209 /len=4089                         | KIAA0<br>854 | KIAA0854 protein  | 8q24.1<br>3  |
| 415<br>35_<br>at | Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,869) /gb=AF006484 /gi=2738496 /ug=Hs.3436 /len=1608 | CDK2<br>AP1  | CDK2-associated protein 1                                     | 12q24.<br>31 |
| 415<br>47_<br>at | Cluster Incl. AF047472:Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds /cds=(70,1056) /gb=AF047472 /gi=2921872 /ug=Hs.40323 /len=2585         | BUB3         | BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog | 10q26        |
| 416<br>09_<br>at | Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162   | HLA-<br>DMB  | major histocompatibility complex, class                       | 6p21.3       |

|                    |  |           |   |               |
|--------------------|--|-----------|---|---------------|
| at                 | /len=1362  |           | II, DM beta   |               |
| 416<br>54_<br>at   | Cluster Incl. X02994:Human mRNA for adenosine deaminase (adenosine aminohydrolase, EC 3.5.4.4) /cds=(95,1186) /gb=X02994 /gi=28379 /ug=Hs.1217 /len=1498   | ADA       | adenosine deaminase                                   | 20q12-q13.11  |
| 416<br>60_<br>at   | Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438 | GTSE<br>1 | G-2 and S-phase expressed 1                           | 22q13.2-q13.3 |
| 416<br>94_<br>at   | Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754 /gi=179512 /ug=Hs.1276 /len=1881  | BN51T     | BN51 (BHK21) temperature sensitivity complementing    | 8q21          |
| 417<br>23_<br>s_at | Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216   | HLA-DRB1  | major histocompatibility complex, class II, DR beta 1 | 6p21.3        |
| 417<br>34_<br>at   | Cluster Incl. AB020677:Homo sapiens mRNA for KIAA0870 protein, complete cds /cds=(436,1998) /gb=AB020677 /gi=4240228 /ug=Hs.18166 /len=4484  | KIAA0870  | KIAA0870 protein                                      | 8q24.3        |
| 417<br>47_<br>s_at | Cluster Incl. U49020:Human myocyte-specific enhancer factor 2A (MEF2A) gene, first coding /cds=(142,1662) /gb=U49020 /gi=1197536   |           |   |               |

|                        |  |             |  |                  |
|------------------------|--|-------------|--|------------------|
|                        | /ug=Hs.182280 /len=5329  |             |  |                  |
| 417<br>63_<br>g_a<br>t | Cluster Incl. D64015:Homo sapiens mRNA for T-cluster binding protein, complete cds /cds=(157,954) /gb=D64015 /gi=2281005 /ug=Hs.182741 /len=1737 | TIAL1       | TIA1 cytotoxic granule-associated RNA-binding protein-like 1 | 10q              |
| 417<br>96_<br>at       | Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147         | PLCE2       | phospholipase C, epsilon 2                                   | 3p24.3           |
| 418<br>08_<br>at       | Cluster Incl. AF052102:Homo sapiens clone 23926 mRNA sequence /cds=UNKNOWN /gb=AF052102 /gi=3360409 /ug=Hs.5671 /len=1884                        |             |  |                  |
| 418<br>09_<br>at       | Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244259 /clone_end=3 /gb=AI656421 /gi=4740400 /ug=Hs.5671 /len=566       | MGC4<br>175 | hypothetical protein MGC4175                                 | 7q21.1<br>-q21.2 |
| 418<br>47_<br>at       | Cluster Incl. AA214546:zr92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516       | IL24        | interleukin 24   | 1q32             |
| 432<br>_s_<br>at       | X02883 /FEATURE=cds /DEFINITION=HSTCRAC Human gene for T-cell receptor alpha chain C region  | TRA         | T cell receptor alpha locus                                  | 14q11.2          |
| 484<br>_at             | U59302 /FEATURE= /DEFINITION=HSU59302 Human  | NCOA<br>1   | nuclear receptor coactivator 1                               | 2p23             |

|            |  |           |   |       |
|------------|--|-----------|---|-------|
| _at        | steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds  | 1         | coactivator 1   |       |
| 529<br>_at | U15932 /FEATURE=<br>/DEFINITION=HSU15932 Human<br>dual-specificity protein phosphatase<br>mRNA, complete cds   | DUSP<br>5 | dual specificity<br>phosphatase 5   | 10q25 |
| 538<br>_at | S53911 /FEATURE=<br>/DEFINITION=S53911<br>CD34=glycoprotein expressed in<br>lymphohematopoietic progenitor cells<br>{alternatively spliced, truncated form}<br>[human, UT7, mRNA, 2657 nt] | CD34      | CD34 antigen  | 1q32  |
| 585<br>_at | M30938 /FEATURE=mRNA#2<br>/DEFINITION=HUMKUP Human Ku<br>(p70/p80) subunit mRNA, complete<br>cds   | XRCC<br>5 | "X-ray repair<br>complementing<br>defective repair<br>in Chinese<br>hamster cells 5<br>(double-strand-<br>break rejoining;<br>Ku autoantigen,<br>80kD)" | 2q35  |
| 605<br>_at | L78833 /FEATURE=exon#36<br>/DEFINITION=HUMBRCA1 Human<br>BRCA1, Rho7 and vat1 genes,<br>complete cds, and ipf35 gene, partial<br>cds   |           |   |       |
| 706<br>_at | Glucocorticoid Receptor, Beta  |           |   |       |
| 767<br>_at | AF001548 /FEATURE=mRNA<br>/DEFINITION=HUA001548 Human  |           |   |       |

|                  |   |           |   |                 |
|------------------|---|-----------|---|-----------------|
| _at              | Chromosome 16 BAC clone<br>CIT987SK-A-815A9,<br>sequence complete   |           |   |                 |
| 820<br>_at       | U77604 /FEATURE=<br>/DEFINITION=HSU77604 Homo<br>sapiens microsomal glutathione S-<br>transferase 2 (MGST2) mRNA,<br>complete cds | MGST<br>2 | microsomal<br>glutathione S-<br>transferase 2   | 4q28-<br>q31    |
| 854<br>_at       | S76617 /FEATURE=<br>/DEFINITION=S76617 blk=protein<br>tyrosine kinase [human, B<br>lymphocytes, mRNA, 2608 nt]                    | BLK       | B lymphoid<br>tyrosine kinase   | 8p23-<br>p22    |
| 931<br>_at       | L08177 /FEATURE=<br>/DEFINITION=HUMGPCRB Human<br>EBV induced G-protein coupled<br>receptor (EBI2) mRNA, complete cds             | EBI2      | Epstein-Barr<br>virus induced<br>gene 2<br>(lymphocyte-<br>specific G<br>protein-coupled<br>receptor) | 13q32.<br>3     |
| 932<br>_i_a<br>t | L11672 /FEATURE=<br>/DEFINITION=HUMKRUPZN Human<br>Kruppel related zinc finger protein<br>(HTF10) mRNA, complete cds              | ZNF91     | zinc finger<br>protein 91<br>(HPF7, HTF10)  | 19p13.<br>1-p12 |
| 933<br>_f_<br>at | L11672 /FEATURE=<br>/DEFINITION=HUMKRUPZN Human<br>Kruppel related zinc finger protein<br>(HTF10) mRNA, complete cds              | ZNF91     | zinc finger<br>protein 91<br>(HPF7, HTF10)  | 19p13.<br>1-p12 |
| 958<br>_s_       | Rna Polymerase II, 14.5 Kda Subunit   |           |   |                 |



|   |   |  |  |  |
|---|---|--|--|--|
| at  |   |  |  |  |
| AFF<br>X-<br>HU<br>MR<br>GE/<br>M1<br>009<br>8_<br>M_<br>at | M10098 Human 18S rRNA gene,<br>complete (_5, _M, _3 represent<br>transcript regions 5 prime, Middle, and<br>3 prime respectively) |  |  |  |

Table 22:

*Pairwise Comparisons*

|                       |   |             |              |               |                           |                                  |      |
|-----------------------|---|-------------|--------------|---------------|---------------------------|----------------------------------|------|
| <i>Classification</i> |   | <b>nBM</b>  | <b>CLL</b>   | <b>CML</b>    | <b>ALL</b>                | <b>AML</b>                       |      |
|                       | <b>nBM</b>                                      |             | KIA0952, BNL | IRF4, HLA-DMB | PLSCR1, KCN2<br>KIAA0482* | PLSCR1, CAMP                     | n=8  |
|                       | <b>CLL</b>                                      | 100% (1.00) |              | TBB, HLA-DMB  | NOCA1, US2981*            | POU2AF1,<br>TNFR857              | n=8  |
|                       | <b>CML</b>                                      | 100% (1.00) | 100% (1.00)  |               | CLC, TALDD1               | DEFA3, LCN2,<br>SOP28*           | n=10 |
|                       | <b>ALL</b>                                      | 100% (0.97) | 100% (1.00)  | 100% (1.00)   |                           | OS-8*, LEF1, MSF,<br>PP08, APLE2 | n=18 |
|                       | <b>AML</b>                                      | 100% (1.00) | 100% (1.00)  | 100% (0.96)   | 97% (0.95)                |                                  | n=59 |
|                       |   | n=8         | n=8          | n=10          | n=18                      | n=59                             |      |
|                       | % = accuracy in leave-one-out cross validation. |             |              |               |                           |                                  |      |
|                       | () = confidence.                                |             |              |               |                           |                                  |      |

Table 23:

| Golub  |                 |    |                | diffgenes            |                 |    |                |
|--|-----------------|----|----------------|----------------------|-----------------|----|----------------|
|  |                 |    |                |                      |                 |    |                |
| A - Samples: 18 / 85                         |                 |    |                | A - samples: 18 / 85 |                 |    |                |
| Accuracy 0,87                                |                 |    |                | accuracy 0,96        |                 |    |                |
| Confidence 0,77                              |                 |    |                | confidence 0,88      |                 |    |                |
| Failed 6,19,22,26,78,79,80,81,82,83,84,85,99 |                 |    |                | failed 5,6,19,22     |                 |    |                |
| Gene   | Signal-to-noise | p  | decision limit | gene                 | signal-to-noise | p  | decision limit |
| g1   | -1,14           | 0* | 482,01         | g1                   | -1,14           | 0  |                |
| g2   | -1,06           | 0* | 192,17         | g2                   | -1,06           | 0* | 98,50          |
| g3   | -0,97           | 0* | 207,67         | g3                   | -0,97           | 0  |                |
| g4   | 0,94            | 0* | 205,05         | g4                   | 0,94            | 0  |                |
| g5   | -0,93           | 0* | 1818,11        | g5                   | -0,93           | 0  |                |
| g6   | 0,93            | 0* | 451,74         | g6                   | 0,93            | 0  |                |
| g7   | -0,91           | 0* | 23,84          | g7                   | -0,91           | 0  |                |
| g8   | -0,90           | 0* | 225,72         | g8                   | -0,90           | 0  |                |

|     |       |    |         |     |       |    |        |
|-----|-------|----|---------|-----|-------|----|--------|
| g9  | 0,90  | 0* | 43,85   | g9  | 0,90  | 0  |        |
| g10 | 0,89  | 0* | 210,78  | g10 | 0,89  | 0  |        |
| g11 | -0,88 | 0* | 118,63  | g11 | -0,88 | 0  |        |
| g12 | 0,87  | 0* | 55,39   | g12 | 0,87  | 0* | 67,80  |
| g13 | 0,87  | 0* | 127,15  | g13 | 0,87  | 0* | 164,10 |
| g14 | 0,86  | 0* | 222,04  | g14 | 0,86  | 0  |        |
| g15 | 0,85  | 0* | 68,52   | g15 | 0,85  | 0  |        |
| g16 | -0,85 | 0* | 546,97  | g16 | -0,85 | 0  |        |
| g17 | 0,84  | 0* | 1242,77 | g17 | 0,84  | 0  |        |
| g18 | -0,84 | 0* | 162,61  | g18 | -0,84 | 0  |        |
| g19 | -0,83 | 0* | 385,39  | g19 | -0,83 | 0  |        |
| g20 | 0,46  | 0* | 105,38  | g20 | 0,46  | 0  |        |

Table 24:

| Classes             | t(15;17)<br>vs.<br>t(8;21) | t(15;17)<br>vs.<br>inv(16) | inv(16)<br>vs.<br>t(8;21) | inv(16)<br>vs.<br>remainder | t(8;21)<br>vs.<br>remainder | t(15;17)<br>vs.<br>remainder |
|---------------------|----------------------------|----------------------------|---------------------------|-----------------------------|-----------------------------|------------------------------|
| Accuracy            | 1.00                       | 1.00                       | 1.00                      | 1.00                        | 1.00                        | 1.00                         |
| Prediction strength | 0.91                       | 0.96                       | 0.93                      | 0.95                        | 0.98                        | 0.91                         |
| M65066              |                            |                            |                           | -1.52                       |                             |                              |
| AL049933            |                            |                            |                           |                             |                             | -2.12                        |
| AF010310            |                            |                            |                           |                             |                             | 1.89                         |
| N90866              |                            |                            |                           |                             |                             | -2.34                        |
| M26326              | 2.85                       |                            |                           |                             | -2.56                       |                              |

|                 |      |  |       |      |      |  |       |
|-----------------|------|--|-------|------|------|--|-------|
| N99340          |      |  |       | 8.43 |      |  |       |
| M25915          |      |  |       |      |      |  | 1.63  |
| P(g,c) AF013570 |      |  | -6.84 | 7.78 | 6.99 |  |       |
|                 |      |  | 3.08  |      |      |  | 3.08  |
| AI207842        | 3.08 |  |       |      | 6.56 |  |       |
| X16665          |      |  |       | 6.56 |      |  | -2.36 |
| X96719          |      |  |       |      |      |  |       |
| AF013611        | 2.68 |  |       |      |      |  |       |
| W72424          |      |  |       |      |      |  | -2.05 |

Table 25

| GenBank<br>accession<br>No. | Approved<br>UCL/HGNC/HUGO<br>database<br>symbol | Description   | Identified<br>according to<br>Golub et al. | Identified<br>utilizing<br>multiple-tree<br>classifiers |
|-----------------------------|---|---|--|---|
| M65066                      | <i>PRKAR1B</i>                                  | cAMP-dependent protein kinase regulatory subunit RI-beta  | X  |   |
| AL049933                    | <i>GNAI1</i>                                    | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1                       | X  |   |
| AF010310                    | <i>PIG6*</i>                                    | proline oxidase homolog   | X  |   |
| N90866                      | <i>CDW52</i>                                    | CDW52 antigen (CAMPATH-1 antigen)   | X  |   |
| M26326                      | <i>KRT18</i>                                    | keratin, type I cytoskeletal 18   | X  | X   |
| N99340                      | <i>DKFZP586N1922</i><br>*                       | DKFZP586N1922 protein   | X  | X   |
| M25915                      | <i>CLU</i>                                      | clusterin precursor   | X  |   |
| A1207842                    | <i>PTGDS</i>                                    | prostaglandin-h2 d-isomerase precursor  | X  |   |
| X16665                      | <i>HOXB2</i>                                    | homeobox protein hox-b2   | X  | X   |
| X96719                      | <i>CLECSF2</i>                                  | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) | X  | X   |
| AF013611                    | <i>CTSW</i>                                     | cathepsin w (lymphopain) precursor  | X  | X   |
| W72424                      | <i>S100A9</i>                                   | calgranulin b (migration inhibitory factor-related protein 14)  | X  |   |
| AF013570                    | <i>MYH11</i>                                    | myosin heavy chain, smooth muscle isoform   | X  | X   |
| AF001548                    | <i>MYH11</i>                                    | myosin heavy chain, smooth muscle isoform   |  | X   |



|          |                           |   |  |   |
|----------|---------------------------|---|--|---|
| X53742   | <i>FBLN1</i>              | fibulin-1   |  | X |
| U37122   | <i>ADD3</i>               | gamma adducin   |  | X |
| J03853   | <i>ADRA2C</i>             | alpha-2c-1 adrenergic receptor  |  | X |
| Y10183   | <i>ALCAM</i>              | CD166 antigen precursor (activated leukocyte-cell adhesion molecule)                            |  | X |
| AB002313 | <i>PLXNB2</i>             | plexin B2   |  | X |
| X78817   | <i>ARHGAP4</i>            | rho GTPase activating protein 4   |  | X |
| X54486   | <i>SERPING1</i>           | plasma protease c1 inhibitor precursor  |  | X |
| L19872   | <i>AHR</i>                | aryl hydrocarbon receptor   |  | X |
| M15395   | <i>ITGB2</i>              | CD18, integrin beta-2 precursor   |  | X |
| AF045229 | <i>RGS10</i>              | regulator of g-protein signaling 10   |  | X |
| D43638   | <i>CBFA2T1</i>            | MTG8 protein (ETO protein)  |  | X |
| M25280   | <i>SELL</i>               | L-selectin precursor (lymph node homing receptor)   |  | X |
| W25986   | <i>DKFZP564K0822</i><br>* | hypothetical protein DKFZp564K0822  |  | X |
| M36035   | <i>BZRP</i>               | peripheral-type benzodiazepine receptor   |  | X |
| X64624   | <i>POU4F1</i>             | brain-specific homeobox/pou domain protein 3a   |  | X |
| M18728   | <i>CEACAM6</i>            | carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) |  | X |
| M77349   | <i>TGFB1</i>              | transforming growth factor-beta induced protein ig-h3 precursor                                 |  | X |

|        |          |  |  |   |
|--------|----------|--|--|---|
| M80899 | AHNAK    | neuroblast differentiation associated protein ahnak  |  | X |
| M13560 | CD74     | CD74 antigen, (invariant polypeptide of major histocompatibility complex, class II antigen-associated) |  | X |
| X62744 | HLA-DMA  | major histocompatibility complex, class II, DM alpha, RING6  |  | X |
| M32578 | HLA-DRB1 | HLA class II histocompatibility antigen, dr-1(dw14) beta chain precursor                               |  | X |
| X00457 | HLA-DPA1 | HLA class II histocompatibility antigen, dp alpha chain precursor                                      |  | X |
| J00194 | HLA-DRA  | HLA class II histocompatibility antigen, dr alpha chain precursor                                      |  | X |

**Table 26: Comparisons of protein expression and mRNA abundance in acute myeloid leukemia as assessed by flow cytometry and microarray analysis**

| Antigen         | Number of comparisons | Both FC and MA positive      | Both FC and MA negative | MA positive and FC negative     | FC positive and MA negative |
|-----------------|-----------------------|------------------------------|-------------------------|---------------------------------|-----------------------------|
| Myeloperoxidase | 25                    | 25                           | -                       | -                               | -                           |
| CD13            | 25                    | 24                           | -                       | -                               | 1                           |
| CD33            | 25                    | 24                           | -                       | -                               | 1                           |
| CD45            | 21                    | 21                           | -                       | -                               | -                           |
| HLA-DR          | 10                    | 10                           | -                       | -                               | -                           |
| CD135           | 4                     | 3                            | -                       | 1                               | -                           |
| CD61            | 19                    | -                            | 19                      | -                               | -                           |
| CD10            | 15                    | -                            | 15                      | -                               | -                           |
| CD235a          | 14                    | -                            | 12                      | 2                               | -                           |
| NG2             | 11                    | -                            | 11                      | -                               | -                           |
| CD22            | 5                     | -                            | 5                       | -                               | -                           |
| CD133           | 4                     | -                            | 4                       | -                               | -                           |
| CD79a           | 2                     | -                            | 1                       | 1                               | -                           |
| CD14            | 23                    | 6                            | 14                      | 3                               | -                           |
| CD34            | 22                    | 17                           | 4                       | 1                               | -                           |
| CD2             | 22                    | 16                           | 3                       | 3                               | -                           |
| CD7             | 22                    | 14                           | 8                       | -                               | -                           |
| CD15            | 19                    | 15                           | 1                       | 3                               | -                           |
| CD3             | 9                     | 4                            | 4                       | 1                               | -                           |
| Lactoferrin     | 13                    | 8                            | 2                       | 3                               | -                           |
| CD116           | 6                     | 4                            | 2                       | -                               | -                           |
| CD11b           | 7                     | 5                            | 2                       | -                               | -                           |
| CD19            | 12                    | 5                            | 2                       | 5                               | -                           |
| CD36            | 22                    | 2                            | 14                      | -                               | 6                           |
| CD38            | 9                     | 4                            | 1                       | -                               | 4                           |
| CD4             | 18                    | 6                            | 7                       | 2                               | 3                           |
| CD56            | 23                    | 2                            | 17                      | -                               | 4                           |
| CD64            | 23                    | 15                           | 4                       | 3                               | 1                           |
| TdT             | 20                    | -                            | 17                      | 2                               | 1                           |
| <b>Total</b>    | <b>450 (100%)</b>     | <b>230 (51.1%)</b>           | <b>169 (37.6%)</b>      | <b>30 (6.7%)</b>                | <b>21 (4.7%)</b>            |
|                 |                       | <b>399 (88.7%) congruent</b> |                         | <b>51 (11.4%) not congruent</b> |                             |

Protein expression and mRNA abundance were compared in 25 patients. "Number of 5 comparisons" indicates the number of patients analyzed for the respective antigens (maximum number, 25 patients)

Table 27

| Affymetrix_ID | Description_microarray  | Symbol        | Description_NetAffx                       | Chromosome    |
|---------------|---|---------------|---|---------------|
| 1087_at       | M60459 /FEATURE=<br>/DEFINITION=HUMERYTH Human<br>erythropoietin receptor mRNA, complete cds  | EPOR          | erythropoietin receptor                   | 19p13.3-p13.2 |
| 1747_at       | AD000092 /FEATURE=cds#2<br>/DEFINITION=CH19HHR23 Homo sapiens<br>DNA from chromosome 19p13.2 cosmids<br>R31240, R30272 and R28549 containing the<br>EKLF, GCDH, CRTC, and RAD23A genes,<br>genomic sequence | unknown cDNA* | ?   |               |
| 1752_at       | AD000092 /FEATURE=cds#6<br>/DEFINITION=CH19HHR23 Homo sapiens<br>DNA from chromosome 19p13.2 cosmids<br>R31240, R30272 and R28549 containing the<br>EKLF, GCDH, CRTC, and RAD23A genes,<br>genomic sequence | unknown cDNA* | ?   |               |
| 180_at        | S82470 /FEATURE= /DEFINITION=S82470<br>BB1=malignant cell expression-enhanced<br>gene/tumor progression-enhanced gene<br>[human, UM-UC-9 bladder carcinoma cell<br>line, mRNA, 1897 nt]                     | LENG4         | leukocyte receptor cluster (LRC) member 4 | 19q13.4       |
| 206_at        | M84424 /FEATURE=expanded_cds<br>/DEFINITION=HUMCTSE09 Human<br>cathepsin E (CTSE) gene, exon 9 and  | CTSE          | cathepsin E                               |               |

| complete cds |  |   |
|--------------|--|---|
| 31381_       | Cluster Incl. AF076483:Homo sapiens<br>peptidoglycan recognition protein precursor<br>(PGRP) mRNA, complete cds /cds=(44,634)<br>at /gb=AF076483 /gi=3342532 /ug=Hs.137583<br>/len=690 | PGLYRP<br>peptidoglycan<br>recognition<br>protein<br>19q13.2-<br>q13.3            |
| 31682_       | Cluster Incl. D32039:Human pgH3 mRNA for<br>proteoglycan PG-M(V3), complete cds<br>s_at /cds=(105,2072) /gb=D32039 /gi=1008912<br>/ug=Hs.234753 /len=2087                              | CSPG2<br>chondroitin<br>sulfate<br>proteoglycan 2<br>(versican)<br>5q14.3         |
| 31749_       | Cluster Incl. Z98744:histone H2A<br>f_at /cds=(7,399) /gb=Z98744 /gi=3080457<br>/ug=Hs.131954 /len=499   | H2AFN<br>H2A histone<br>family, member<br>N<br>6p22-p21.3                         |
| 32323_       | Cluster Incl. M63582:Human<br>preprothyrotropin-releasing hormone gene<br>at /cds=(8,736) /gb=M63582 /gi=190297<br>/ug=Hs.182231 /len=1457   | TRH<br>thyrotropin-<br>releasing<br>hormone<br>3q13.3-q21                         |
| 33093_       | Cluster Incl. AF077346:Homo sapiens<br>interleukin-18 receptor accessory protein-like<br>at mRNA, complete cds /cds=(483,2282)<br>/gb=AF077346 /gi=3851059 /ug=Hs.158315<br>/len=2681  | IL18RAP<br>interleukin 18<br>receptor<br>accessory<br>protein<br>2p24.3-<br>p24.1 |
| 33584_       | Cluster Incl. U35146:Human p56 KKIAMRE<br>protein kinase (KKIAMRE), complete cds<br>at /cds=(0,1481) /gb=U35146 /gi=1517819<br>/ug=Hs.158512 /len=1482                                 | CDKL2<br>cyclin-<br>dependent<br>kinase-like 2<br>(CDC2-related<br>kinase)<br>4   |
| 34110_       | Cluster Incl. AF010310:Homo sapiens p53<br>g_at induced protein mRNA, partial cds<br>/cds=(0,761) /gb=AF010310 /gi=2415296   | PIG6<br>proline oxidase<br>homolog  |

|        |   |  |          |   |         |
|--------|---|--|----------|---|---------|
|        |   | /ug=Hs.211605 /len=888   |          |   |         |
|        |   | Cluster Incl. AL049651:Human DNA<br>sequence from clone 753D10 on<br>chromosome 20 Contains genes for            |          |   |         |
| 34139_ | SSTR4(somatostatin receptor 4) and  |  | SSTR4    | somatostatin<br>receptor 4  | 20p11.2 |
| at     | THBD(thrombomodulin), ESTs, STSs, GSSs<br>and CpG islands /cds=(98,1264)<br>/gb=AL049651 /gi=4741619 /ug=Hs.226015<br>/len=1427 |  |          |   |         |
|        |   | Cluster Incl. AL039458:DKFZp434N0910_s1<br>Homo sapiens cDNA, 3 end  |          |   |         |
| 34800_ | /clone=DKFZp434N0910 /clone_end=3   |  | LIG1     | ortholog of<br>mouse integral<br>membrane<br>glycoprotein<br>LIG-1          |         |
| at     | /gb=AL039458 /gi=5408506 /ug=Hs.4193<br>/len=849  |  |          |   |         |
|        |   | Cluster Incl. M15059:Human Fc-epsilon<br>receptor (IgE receptor) mRNA, complete cds                              |          |   |         |
| 34960_ | g_at (H107 epitope) /cds=(213,1178) /gb=M15059<br>/gi=182447 /ug=Hs.1416 /len=1530  |  | FCER2    | Fc fragment of<br>IgE, low affinity<br>II, receptor for<br>(CD23A)          | 19p13.3 |
|        |   | Cluster Incl. AB009598:Homo sapiens<br>mRNA for glucuronyltransferase I, complete                                |          |   |         |
| 35179_ | at cds /cds=(29,1036) /gb=AB009598<br>/gi=3892639 /ug=Hs.26492 /len=1441  |  | B3GAT3   | beta-1,3-<br>glucuronyltrans<br>ferase 3<br>(glucuronosyltr<br>ansferase I) | 11q12.2 |
|        |   | Cluster Incl. AC004410:Homo sapiens<br>chromosome 19, fosmid 39554   |          |   |         |
| 35426_ | at /cds=(0,1196) /gb=AC004410 /gi=2959558<br>/ug=Hs.167352 /len=1197  |  | LOC56928 | hypothetical<br>protein from<br>EUROIMAGE<br>42353                          | 19p13.3 |
|        |   | Cluster Incl. AI041180:ov77e05.x1 Homo<br>sapiens cDNA, 3 end /clone=IMAGE-<br>1643360 /clone_end=3 /gb=AI041180 |          |   |         |
| 35552_ | at  |  | PCYT1B   | phosphate<br>cytidyltransfer<br>ase 1, choline,                             | Xp22.22 |

|        |   |               |                                    |          |
|--------|---|---------------|------------------------------------|----------|
|        | /gi=3280374 /ug=Hs.132794 /len=810  |               | beta isoform                       |          |
| 35766_ | Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343)   | KRT18         | keratin 18                         | 12q13    |
| at     | /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412  |               |                                    |          |
| 36021_ | Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN                  | LEF1          | lymphoid enhancer-binding factor 1 | 4q23-q25 |
| at     | /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419   |               |                                    |          |
| 36052_ | Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 | ADD2          | adducin 2 (beta)                   | 2p14-p13 |
| at     | /ug=Hs.4852 /len=1284   |               |                                    |          |
| 36095_ | Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074   | DKFZP586N1922 | DKFZP586N1922 protein              | 19q13.1  |
| at     | /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110  |               |                                    |          |
| 36372_ | Cluster Incl. U51333:Human hexokinase III (HK3) mRNA, complete cds /cds=(74,2845)                                     | HK3           | hexokinase 3 (white cell)          | 5q35.2   |
| at     | /gb=U51333 /gi=1255787 /ug=Hs.159237 /len=3049  |               |                                    |          |
| 36464_ | Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323  | SGP28         | specific granule protein (28 kDa)  | 6p12.3   |
| at     | /gi=1213612 /ug=Hs.54431 /len=2124  |               |                                    |          |
| 36657_ | Cluster Incl. AA883870:am26f01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1467961 /clone_end=3 /gb=AA883870             | APOC2         | apolipoprotein C-II                | 19q13.2  |
| at     | /gi=2993400 /ug=Hs.75615 /len=599   |               |                                    |          |

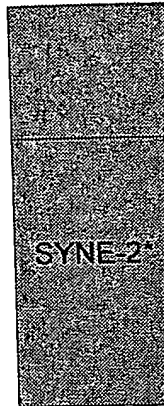
|        |  |           |  |          |
|--------|--|-----------|--|----------|
| 36710_ | Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) at /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615                    | CAMP      | cathelicidin antimicrobial peptide   | 3p21.3   |
| 36780_ | Cluster Incl. M25915:Human complement cytolysis inhibitor (CLI) mRNA, complete cds at /cds=(198,1544) /gb=M25915 /gi=180619 /ug=Hs.75106 /len=1651 | CLU       | clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) | 8p21-p12 |
| 38487_ | Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) at /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777                      | FLJ12442  | hypothetical protein FLJ12442  |          |
| 38975_ | Cluster Incl. AF062534:Homo sapiens genethonin 1 mRNA, complete cds at /cds=(127,1203) /gb=AF062534 /gi=3851521 /ug=Hs.109590 /len=2340            | GENX-3414 | genethonin 1   | 4q24-q25 |
| 39070_ | Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds at /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767        | SNL       | singed (Drosophila)-like (sea urchin fascin homolog like)  | 7p22     |
| 39221_ | Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds                                  | LILRB2    | leukocyte immunoglobulin-like receptor,  | 19q13.4  |



|                |   |          |  |             |
|----------------|---|----------|--|-------------|
|                | /cds=(208,2001) /gb=AF004231 /gi=2343110<br>/ug=Hs.22405 /len=2863  |          | subfamily B<br>(with TM and<br>ITIM domains),<br>member 2                          |             |
| 39307_<br>s_at | Cluster Incl. X81637:H.sapiens clathrin light<br>chain b gene /cds=UNKNOWN /gb=X81637<br>/gi=963046 /ug=Hs.239782 /len=5938                               | CLTB     | clathrin, light<br>polypeptide   | 4q21-qter   |
| 39775_<br>at   | Cluster Incl. X54486:Human gene for C1-<br>inhibitor /cds=(60,1562) /gb=X54486<br>/gi=29534 /ug=Hs.151242 /len=1827                                       | SERPINC1 | complement<br>component 1<br>inhibitor   | 11q12-q13.1 |
| 40282_<br>s_at | Cluster Incl. M84526:Human<br>adipsin/complement factor D mRNA,<br>complete cds /cds=(54,740) /gb=M84526<br>/gi=178625 /ug=Hs.155597 /len=1071            | DF       | D component<br>of complement<br>(adipsin)  | 19p13.3     |
| 40365_<br>at   | Cluster Incl. M63904:Human G-alpha 16<br>protein mRNA, complete cds<br>/cds=(219,1343) /gb=M63904 /gi=182891<br>/ug=Hs.73797 /len=2060                    | GNA15    | guanine<br>nucleotide<br>binding protein<br>(G protein),<br>alpha 15 (Gq<br>class) | 19p13.3     |
| 40763_<br>at   | Cluster Incl. U85707:Human leukemogenic<br>homolog protein (MEIS1) mRNA, complete<br>cds /cds=(65,1237) /gb=U85707<br>/gi=2058550 /ug=Hs.170177 /len=2511 | MEIS1    | Meis1 (mouse)<br>homolog   | 2p14-p13    |
| 41045_<br>at   | Cluster Incl. U77643:Homo sapiens K12<br>protein precursor mRNA, complete cds<br>/cds=(118,864) /gb=U77643 /gi=2062390<br>/ug=Hs.95655 /len=2000          | SECTM1   | secreted and<br>transmembrane<br>1   | 17q25       |
| 41448_<br>at   | Cluster Incl. AC004080:Homo sapiens PAC<br>clone DJ0170019 from 7p15-p21  | HOXA10   | homeo box A10  | 7p15-p14    |

at /cds=(0,1247) /gb=AC004080 /gi=2822164  
/ug=Hs.110637 /len=1248

Cluster Incl. AL080133:Homo sapiens  
mRNA; cDNA DKFZp434G173 (from clone  
41815\_ DKFZp434G173) /cds=(122,3400)  
at /gb=AL080133 /gi=5262573 /ug=Hs.57749  
/len=4307



synaptic nuclei

expressed

gene 2

14q23.2

Table 28a

| classes                | BM - t(8;21)     | BM -<br>t(15;17) | BM -<br>inv(16)  | BM -<br>t(11q23)/ML<br>L | BM - AML         |
|------------------------|------------------|------------------|------------------|--------------------------|------------------|
| accuracy               | 1.00             | 1.00             | 1.00             | 1.00                     | 1.00             |
| prediction<br>strenght | 0.88             | 0.91             | 0.99             | 0.89                     | 0.89             |
| Symbol                 | P(g,c)<br>values | P(g,c)<br>values | P(g,c)<br>values | P(g,c)<br>values         | P(g,c)<br>values |
| EPOR                   |                  | 7.36             | 7.36             |                          | 2.74             |
| unknown cDNA*          |                  | -6.46            |                  |                          |                  |
| unknown cDNA*          |                  | -2.76            |                  |                          |                  |
| LENG4*                 |                  | -2.92            |                  |                          |                  |
| CTSE                   |                  | 3.35             |                  | 2.51                     | 2.39             |
| PGLYRP                 |                  | 7.39             |                  |                          |                  |
| CSPG2                  |                  | 7.39             |                  |                          |                  |
| H2AFN                  |                  |                  |                  | -5.02                    |                  |
| IRH                    | -2.12            |                  |                  |                          |                  |

|                    |      |       |       |       |       |
|--------------------|------|-------|-------|-------|-------|
| IL18RAP            |      |       |       | 4.79  |       |
| CDKL2              |      | -3.12 |       |       |       |
| PIG6               |      | -2.92 |       |       |       |
| SSTR4              |      | 16.61 |       |       |       |
| LIG1               |      |       |       |       | 3.06  |
| FCER2              |      | 4.72  |       |       |       |
| B3GAT3             |      | -2.04 |       |       |       |
| LOC56928*          |      |       |       | -8.39 | -1.70 |
| PCYT1B             | 3.56 |       |       |       |       |
| KRT18              |      | -3.02 |       |       |       |
| LEF1               |      |       |       | 3.26  | 3.26  |
| ADD2               |      | 5.63  |       |       |       |
| DKFZP586N192<br>2* |      |       | -8.84 |       |       |
| HK3                |      | 6.55  |       |       |       |
| SGP28*             |      |       |       |       | 3.04  |
| APOC2              |      | -5.33 |       | -4.16 |       |
| CAMP               |      | 6.40  |       |       |       |
| CLU                |      | -2.71 |       |       |       |

|            |  |       |  |       |       |
|------------|--|-------|--|-------|-------|
| FLJ12442*  |  | -2.16 |  |       |       |
| GENX-3414* |  |       |  | 1.97  |       |
| SNL        |  | -3.64 |  |       |       |
| LILRB2     |  | 9.75  |  |       |       |
| CLTB       |  |       |  | -4.38 |       |
| SERPING1   |  | -2.48 |  |       |       |
| DF         |  | -2.95 |  |       | -1.73 |
| GNA15      |  | -2.69 |  |       |       |
| MEIS1      |  |       |  | -4.22 |       |
| SECTM1     |  | 7.07  |  |       |       |
| HOXA10     |  |       |  | -3.18 |       |
| SYNE-2*    |  |       |  | 3.36  |       |

Table 28b: In total 269 cases with leukemia or normal bone marrow (BM) were analyzed. 248 of 269 (92.2%) cases were assigned to the correct leukemia type in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

|                 | ALL<br>t(4;11) | ALL<br>t(8;14) | ALL B<br>not Ph | ALL<br>Ph | T-<br>ALL | AML<br>+8 | AML<br>complex | AML<br>normal | AML<br>t(8;21) | AML<br>t(15;17) | AML<br>inv(16) | AML<br>MLL | CLL | CML | normal<br>BM | total | sensitivity<br>% | specificity<br>% |
|-----------------|----------------|----------------|-----------------|-----------|-----------|-----------|----------------|---------------|----------------|-----------------|----------------|------------|-----|-----|--------------|-------|------------------|------------------|
| ALL<br>t(4;11)  | 9              |                |                 |           |           |           |                |               |                |                 |                |            |     |     |              | 9     | 100.00           | 90.00            |
| ALL<br>t(8;14)  |                | 3              |                 |           |           |           | 1              |               |                |                 |                |            |     |     |              | 4     | 75.00            | 100.00           |
| ALL B not Ph    |                |                | 8               | 1         |           |           |                |               |                |                 |                |            |     |     |              | 9     | 88.89            | 80.00            |
| ALL Ph          |                |                | 1               | 14        |           |           |                |               |                |                 |                |            |     |     |              | 15    | 93.33            | 87.50            |
| T-ALL           |                |                |                 |           | 8         |           | 1              |               |                |                 |                |            |     |     |              | 9     | 88.89            | 100.00           |
| AML +8          |                |                |                 |           |           | 5         |                | 4             |                |                 |                |            |     |     |              | 10    | 0.60             | 100.00           |
| AML<br>complex  | 1              |                |                 |           |           |           | 30             | 3             |                |                 |                |            |     |     | 1            | 36    | 83.33            | 90.91            |
| AML<br>normal   |                |                |                 | 1         |           |           | 1              | 58            |                |                 |                | 2          |     |     |              | 62    | 93.55            | 85.29            |
| AML<br>t(8;21)  |                |                |                 |           |           |           |                |               | 2              |                 |                |            |     |     |              | 13    | 100.00           | 100.00           |
| AML<br>t(15;17) |                |                |                 |           |           |           |                |               |                | 20              |                |            |     |     |              | 20    | 100.00           | 100.00           |
| AML<br>inv(16)  |                |                |                 |           |           |           |                |               |                |                 | 12             |            |     |     |              | 12    | 100.00           | 100.00           |
| AML             |                |                |                 |           |           |           |                |               |                |                 |                | 13         |     |     |              | 15    | 86.67            | 86.67            |
| MLL             |                |                |                 |           |           |           |                |               |                |                 |                |            | 3   |     |              | 32    | 96.88            | 1.00             |
| CLL             |                |                |                 |           |           |           |                |               |                |                 |                |            |     | 14  |              | 14    | 100.00           | 100.00           |
| CML             |                |                |                 |           |           |           |                |               |                |                 |                |            |     |     |              | 9     | 100.00           | 90.00            |
| normal<br>BM    |                |                |                 |           |           |           |                |               |                |                 |                |            |     |     |              | 10    |                  |                  |
| total           | 10             | 3              | 10              | 16        | 8         | 6         | 33             | 68            | 13             | 20              | 12             | 15         | 31  | 14  | 10           | 269   |                  |                  |

Table 28c: In total 3766 individual assignments of leukemia and normal bone marrow were analyzed. 3745 of 3766 assignments (99.4%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

|                 | ALL<br>t(4;11) | ALL<br>t(8;14) | ALL B<br>not Ph | ALL B<br>Ph | T-<br>ALL | AML<br>+8 | AML<br>complex | AML<br>normal | AML<br>t(8;21) | AML<br>t(15;17) | AML<br>inv(16) | AML<br>MLL | CLL | CML | normal<br>BM | total | sensitivity<br>% | specificity<br>% |
|-----------------|----------------|----------------|-----------------|-------------|-----------|-----------|----------------|---------------|----------------|-----------------|----------------|------------|-----|-----|--------------|-------|------------------|------------------|
| ALL<br>t(4;11)  | 126            |                |                 |             |           |           |                |               |                |                 |                |            |     |     |              | 126   | 100.00           | 99.21            |
| ALL<br>t(8;14)  |                | 55             |                 |             |           |           | 1              |               |                |                 |                |            |     |     |              | 56    | 98.21            | 100.00           |
| ALL B<br>not Ph |                |                | 135             |             |           |           |                |               |                |                 |                |            |     |     |              | 126   | 99.21            | 98.43            |
| ALL B<br>Ph     |                |                |                 | 1           |           |           |                |               |                |                 |                |            |     |     |              | 210   | 99.52            | 99.05            |
| T-ALL           |                |                |                 |             | 125       |           | 1              |               |                |                 |                |            |     |     |              | 140   | 99.21            | 100.00           |
| AML<br>+8       |                |                |                 |             |           | 136       |                | 4             |                |                 |                |            |     |     |              |       | 97.14            | 100.00           |
| AML<br>complex  | 1              |                |                 |             |           |           | 198            | 3             |                |                 |                |            |     |     | 1            | 504   | 98.81            | 99.40            |
| AML<br>normal   |                |                |                 | 1           |           |           | 1              | 864           |                |                 |                | 2          |     |     |              | 868   | 99.54            | 98.86            |
| AML<br>t(8;21)  |                |                |                 |             |           |           |                |               | 182            |                 |                |            |     |     |              | 182   | 100.00           | 100.00           |
| AML<br>t(15;17) |                |                |                 |             |           |           |                |               |                | 280             |                |            |     |     |              | 280   | 100.00           | 100.00           |
| AML<br>inv(16)  |                |                |                 |             |           |           |                |               |                |                 | 168            |            |     |     |              | 168   | 100.00           | 100.00           |
| AML<br>MLL      |                |                |                 |             |           |           |                | 2             |                |                 |                | 208        |     |     |              | 210   | 99.05            | 99.05            |
| CLL             |                |                |                 |             |           |           |                | 1             |                |                 |                |            | 447 |     |              | 448   | 99.78            | 100.00           |
| CML             |                |                |                 |             |           |           |                |               |                |                 |                |            |     | 196 |              | 196   | 100.00           | 100.00           |
| normal<br>BM    |                |                |                 |             |           |           |                |               |                |                 |                |            |     |     |              | 126   | 100.00           | 99.21            |
| total           | 127            | 55             | 127             | 211         | 125       | 136       | 501            | 874           | 182            | 280             | 168            | 210        | 447 | 196 | 127          | 3766  |                  |                  |

Table 29

**Analysis of the listed 14 leukemia subgroups and normal bone marrow (BM) according to the method as described by Golub et al. In pairwise comparison**

|              | N  |
|--------------|----|
| ALL t(4;11)  | 9  |
| ALL t(8;14)  | 4  |
| ALL B not Ph | 9  |
| ALL Ph       | 15 |
| T-ALL        | 9  |
| AML +8       | 10 |
| AML complex  | 36 |
| AML normal   | 62 |
| AML t(8;21)  | 13 |
| AML t(15;17) | 20 |
| AML inv(16)  | 12 |
| AML MLL      | 15 |
| CLL          | 32 |
| CML          | 14 |
| normal BM    | 9  |



|                           |                   |                  |                |             |
|---------------------------|-------------------|------------------|----------------|-------------|
| ALL t(4;11) vs. all other |                   | samples: 9 / 260 |                |             |
| accuracy                  | 1                 |                  |                |             |
| confidence                | 0.983255511396901 |                  |                |             |
| gene                      | signal-to-noise   | p                | decision limit | gene symbol |
| 215925_s_at               | 2.15211119031413  | 0                |                |             |
| 225592_at                 | 2.10479676639873  | 0                |                | NRM         |
| 205821_at                 | 2.06781828794101  | 0                |                | D12S2489E   |
| 209168_at                 | 2.03682741085015  | 0                |                | GPM6B       |
| 225563_at                 | 2.0365845909197   | 0                |                |             |
| 209170_s_at               | 1.99341681464758  | 0                |                | GPM6B       |
| 219033_at                 | 1.98127277039877  | 0*               | 3296.75        | FLJ21308    |
| 227407_at                 | 1.9806645400311   | 0*               | 2368.95        |             |
| 226496_at                 | 1.94883167321783  | 0                |                |             |
| 219463_at                 | 1.92861464656998  | 0                |                | C20orf103   |
| 203796_s_at               | 1.90484126349741  | 0                |                | BCL7A       |
| 210934_at                 | 1.78273564893858  | 0                |                | BLK         |
| 221969_at                 | 1.72749112194125  | 0                |                | PAX5        |
| 239393_at                 | 1.72516948033426  | 0                |                |             |
| 238750_at                 | 1.71981673787555  | 0                |                |             |
| 239214_at                 | 1.67607810398359  | 0*               | 645.75         |             |
| 218469_at                 | 1.65073049955565  | 0                |                | CKTSF1B1    |
| 226244_at                 | 1.64755028976206  | 0                |                |             |
| 218384_at                 | 1.64357646019602  | 0                |                | CRHSP-24    |
| 209815_at                 | 1.64023870547228  | 0                |                | PTCH        |

t(4;11) vs. t(15;17) samples: 9 / 20

accuracy 1

confidence 1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 221969_at   | 5.83664657385464  | 0* | 1301           | PAX5        |
| 207697_x_at | 5.35854600658567  | 0  |                | LILRB2      |
| 203948_s_at | -5.11890143327711 | 0  |                | MPO         |
| 224918_x_at | -4.9355306862525  | 0  |                | MGST1       |
| 203949_at   | -4.8364973202297  | 0  |                | MPO         |
| 231736_x_at | -4.46563746824662 | 0  |                | MGST1       |
| 235101_at   | 4.28876186377802  | 0  |                | KIAA1014    |
| 202481_at   | 4.05195275593644  | 0  |                | SDR1        |
| 219463_at   | 3.9253737114322   | 0  |                | C20orf103   |
| 201540_at   | 3.81769665767171  | 0  |                | FHL1        |
| 238583_at   | -3.81099135622948 | 0  |                |             |
| 205382_s_at | -3.80101585016411 | 0  |                | DF          |
| 226878_at   | 3.74369099536436  | 0  |                |             |
| 210934_at   | 3.72127171897839  | 0  |                | BLK         |
| 226545_at   | 3.69021106148297  | 0  |                |             |
| 38487_at    | -3.54247992575908 | 0  |                | FLJ12442    |
| 220798_x_at | -3.50808230625528 | 0  |                | FLJ11535    |
| 232201_at   | 3.50091671488931  | 0  |                | NKD2        |
| 204069_at   | 3.4252967216987   | 0  |                | MEIS1       |
| 244261_at   | 3.40910490910101  | 0  |                |             |

|                            |                        |          |                       |                    |
|----------------------------|------------------------|----------|-----------------------|--------------------|
| <b>t(4;11) vs. inv(16)</b> | <b>samples: 9 / 12</b> |          |                       |                    |
| accuracy                   | 1                      |          |                       |                    |
| confidence                 | 1                      |          |                       |                    |
| <b>gene</b>                | <b>signal-to-noise</b> | <b>p</b> | <b>decision limit</b> | <b>gene symbol</b> |
| 225653_at                  | -6.57614058007186      | 0*       | 129.2                 |                    |
| 221969_at                  | 5.83664657385464       | 0        |                       | PAX5               |
| 231259_s_at                | -5.68009935369819      | 0        |                       | CCND2              |
| 203949_at                  | -4.47845706407372      | 0        |                       | MPO                |
| 200951_s_at                | -4.24994685464806      | 0        |                       | CCND2              |
| 219463_at                  | 3.9253737114322        | 0        |                       | C20orf103          |
| 203948_s_at                | -3.82832616186979      | 0        |                       | MPO                |
| 200953_s_at                | -3.81507848947069      | 0        |                       | CCND2              |
| 217979_at                  | 3.7506313191621        | 0        |                       | NET-6              |
| 210934_at                  | 3.72127171897839       | 0        |                       | BLK                |
| 204214_s_at                | -3.64249678228396      | 0        |                       | RAB32              |
| 203973_s_at                | -3.54203246324105      | 0        |                       | CEBPD              |
| 232201_at                  | 3.50091671488931       | 0        |                       | NKD2               |
| 216860_s_at                | 3.46199526723217       | 0        |                       | GDF11              |
| 244261_at                  | 3.40910490910101       | 0        |                       |                    |
| 201360_at                  | -3.40410310063102      | 0        |                       | CST3               |
| 226496_at                  | 3.36372190983709       | 0        |                       |                    |
| 238824_at                  | 3.31690199423555       | 0        |                       |                    |
| 217966_s_at                | -3.29280071064851      | 0        |                       | C1orf24            |
| 38340_at                   | 2.62428006100593       | 0        |                       | HIP12              |

|                                |                        |                 |                       |                    |
|--------------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>ALL t(4;11) vs. AML MLL</b> |                        | samples: 9 / 15 |                       |                    |
| accuracy                       | 1                      |                 |                       |                    |
| confidence                     | 1                      |                 |                       |                    |
| <b>gene</b>                    | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 221969_at                      | 4.924403129677         | 0*              | 1534.5                | PAX5               |
| 226795_at                      | 4.12248256776444       | 0               |                       |                    |
| 205821_at                      | 4.05458217339808       | 0               |                       | D12S2489E          |
| 201360_at                      | -3.44934876199386      | 0               |                       | CST3               |
| 244261_at                      | 3.40910490910101       | 0               |                       |                    |
| 217979_at                      | 3.33945130505483       | 0               |                       | NET-6              |
| 204215_at                      | 3.27742574573237       | 0               |                       | MGC4175            |
| 211404_s_at                    | -3.1044343641572       | 0               |                       | APLP2              |
| 217223_s_at                    | 3.09813118817326       | 0               |                       |                    |
| 206255_at                      | 3.06828641368978       | 0               |                       | BLK                |
| 214875_x_at                    | -2.95163557135368      | 0               |                       | APLP2              |
| 201828_x_at                    | -2.94392957130376      | 0               |                       | CXX1               |
| 208702_x_at                    | -2.9259192302265       | 0               |                       | APLP2              |
| 208456_s_at                    | 2.83112443648876       | 0               |                       | RRAS2              |
| 219229_at                      | -2.78106365052986      | 0               |                       | SLC21A11           |
| 210487_at                      | 2.65572482698711       | 0               |                       | DNTT               |
| 210192_at                      | 2.63764031456982       | 0               |                       | ATP8A1             |
| 226496_at                      | 2.63678458715383       | 0               |                       |                    |
| 203796_s_at                    | 2.63294411410401       | 0               |                       | BCL7A              |
| 212207_at                      | 2.62364024475935       | 0               |                       | KIAA1025           |

## ALL t(4;11) vs. CLL

samples: 9 / 32

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

210045\_at

6.76734853184964

0\*

142.15

IDH2

204798\_at

4.99101493214162

0

MYB

225592\_at

4.17686594916951

0

NRM

202503\_s\_at

4.02396247600866

0

KIAA0101

219463\_at

3.9253737114322

0

C20orf103

201540\_at

3.7195174107357

0

FHL1

226545\_at

3.4985271993093

0

223276\_at

3.36058308258119

0

NID67

209267\_s\_at

3.33868760455037

0

LOC64116

201416\_at

3.27673886279907

0

SOX4

224710\_at

3.27404618682988

0

RAB34

218384\_at

3.26299093107225

0

CRHSP-24

209365\_s\_at

3.22987740485106

0

ECM1

219869\_s\_at

3.18151227716348

0

LOC64116

218942\_at

-3.1335063798458

0

FLJ22055

209825\_s\_at

3.12344649016037

0

UMPK

201417\_at

3.10175892236352

0

238022\_at

3.08645149251292

0

212281\_s\_at

3.07915047956129

0

MAC30

204069\_at

3.04751039522855

0

MEIS1

| ALL t(4;11) vs. CML |                   | samples: 9 / 14 |                |             |  |
|---------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy            | 1                 |                 |                |             |  |
| confidence          | 1                 |                 |                |             |  |
| gene                | signal-to-noise   | p               | decision limit | gene symbol |  |
| 221969_at           | 5.83664657385464  | 0*              | 1301           | PAX5        |  |
| 207000_s_at         | 4.65703873448273  | 0               |                | PPP3CC      |  |
| 212484_at           | 4.34689222808594  | 0               |                | MTVR        |  |
| 201485_s_at         | 4.25216281704109  | 0               |                | RCN2        |  |
| 204214_s_at         | -4.24363288728321 | 0               |                | RAB32       |  |
| 203796_s_at         | 4.18407933075926  | 0               |                | BCL7A       |  |
| 218223_s_at         | 4.16804739438629  | 0               |                | LOC51177    |  |
| 226795_at           | 4.12248256776444  | 0               |                |             |  |
| 205821_at           | 4.05458217339808  | 0               |                | D12S2489E   |  |
| 221755_at           | 3.99463418568195  | 0               |                |             |  |
| 219463_at           | 3.9253737114322   | 0               |                | C20orf103   |  |
| 202332_at           | 3.87997129184981  | 0               |                | CSNK1E      |  |
| 210254_at           | -3.85534735854191 | 0               |                |             |  |
| 209619_at           | 3.77477243739775  | 0               |                | CD74        |  |
| 226878_at           | 3.74369099536436  | 0               |                |             |  |
| 205557_at           | -3.71054014877636 | 0               |                | BPI         |  |
| 225713_at           | 3.59398617666668  | 0               |                | KIAA1898    |  |
| 206440_at           | -3.54851691296324 | 0               |                | VELI1       |  |
| 232201_at           | 3.50091671488931  | 0               |                | NKD2        |  |
| 204215_at           | 3.43706276144109  | 0               |                | MGC4175     |  |

## ALL t(4;11) vs. normal BM

samples: 9 / 9

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

201828\_x\_at

-6.82241973614495

0\*

285.3

CXX1

210045\_at

6.76734853184964

0

IDH2

214950\_at

6.24435639089538

0

237431\_at

5.31661820706767

0

225792\_at

-5.04037264761662

0

205624\_at

-4.8793192574965

0

CPA3

201540\_at

4.79436840204501

0

FHL1

204214\_s\_at

-4.53807365704691

0

RAB32

218916\_at

4.52409549429394

0

FLJ23436

200832\_s\_at

-4.29237917192722

0

SCD

203796\_s\_at

4.18407933075926

0

BCL7A

205051\_s\_at

-4.13944949609416

0

KIT

202332\_at

4.13816009401715

0

CSNK1E

228176\_at

-4.13090953290361

0

226795\_at

4.12248256776444

0

208754\_s\_at

4.00220842620578

0

NAP1L1

221755\_at

3.99463418568195

0

228424\_at

-3.92813180248343

0

NAALADASEL

219463\_at

3.9253737114322

0

C20orf103

212967\_x\_at

3.92366867855542

0

NAP1L1

| ALL t(4;11) vs. ALL t(8;14) |                   | samples: 9 / 4 |                |             |  |
|-----------------------------|-------------------|----------------|----------------|-------------|--|
| accuracy                    | 1                 |                |                |             |  |
| confidence                  | 1                 |                |                |             |  |
| gene                        | signal-to-noise   | p              | decision limit | gene symbol |  |
| 210045_at                   | 6.76734853184964  | 0*             | 142.15         | IDH2        |  |
| 240106_at                   | 6.10571301118426  | 0              |                |             |  |
| 202853_s_at                 | -5.88804457870992 | 0              |                | RYK         |  |
| 242434_at                   | -5.60754470569171 | 0              |                |             |  |
| 237431_at                   | 5.31661820706767  | 0              |                |             |  |
| 201540_at                   | 4.94655082712075  | 0              |                | FHL1        |  |
| 215855_s_at                 | 4.71299810202736  | 0              |                |             |  |
| 212357_at                   | 4.18767818184794  | 0              |                | KIAA0280    |  |
| 204798_at                   | 4.12313508850913  | 0              |                | MYB         |  |
| 226795_at                   | 4.12248256776444  | 0              |                |             |  |
| 77508_r_at                  | 4.0317985345148   | 0              |                | FLJ23282    |  |
| 46142_at                    | 3.95748459279267  | 0              |                | FLJ12681    |  |
| 225277_at                   | 3.7552029934786   | 0              |                |             |  |
| 210934_at                   | 3.72127171897839  | 0              |                | BLK         |  |
| 215537_x_at                 | 3.53324247477066  | 0              |                |             |  |
| 232201_at                   | 3.50091671488931  | 0              |                | NKD2        |  |
| 214505_s_at                 | 3.42260996379197  | 0              |                | FHL1        |  |
| 244261_at                   | 3.40910490910101  | 0              |                |             |  |
| 208614_s_at                 | 3.34565043119022  | 0              |                | FLNB        |  |
| 210298_x_at                 | 3.30171221592859  | 0.01           |                | FHL1        |  |



| ALL t(4;11) vs. ALL B not Ph |                   | samples: 9 / 9 |                |             |
|------------------------------|-------------------|----------------|----------------|-------------|
| accuracy                     | 1                 |                |                |             |
| confidence                   | 1                 |                |                |             |
| gene                         | signal-to-noise   | p              | decision limit | gene symbol |
| 237431_at                    | 5.31661820706767  | 0*             | 49             |             |
| 219033_at                    | 3.19032095561144  | 0              |                | FLJ21308    |
| 219463_at                    | 2.69567768562793  | 0              |                | C20orf103   |
| 204069_at                    | 2.54127866831197  | 0              |                | MEIS1       |
| 201105_at                    | 2.30596776500018  | 0              |                | LGALS1      |
| 200907_s_at                  | 2.19034049161844  | 0              |                | KIAA0992    |
| 242414_at                    | 2.08870062415486  | 0              |                |             |
| 222492_at                    | -2.04226084466602 | 0              |                | FLJ21324    |
| 230441_at                    | -2.03717805375485 | 0              |                |             |
| 235291_s_at                  | 2.0210425168076   | 0              |                |             |
| 225592_at                    | 2.01329642963674  | 0              |                | NRM         |
| 200906_s_at                  | 1.9632986862999   | 0              |                |             |
| 201153_s_at                  | 1.93254941630797  | 0              |                | MBNL        |
| 201152_s_at                  | 1.93227192981893  | 0              |                | MBNL        |
| 241985_at                    | -1.91875000661653 | 0              |                |             |
| 213894_at                    | 1.89533012552966  | 0              |                | KIAA0960    |
| 243756_at                    | 1.82938790694615  | 0              |                |             |
| 225563_at                    | 1.82046495626766  | 0              |                |             |
| 232231_at                    | 1.8138577510169   | 0              |                |             |
| 240581_at                    | 1.80942575017411  | 0              |                |             |

| ALL t(4;11) vs. ALL Ph |                   | samples: 9 / 15 |                |             |  |
|------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy               | 1                 |                 |                |             |  |
| confidence             | 1                 |                 |                |             |  |
| gene                   | signal-to-noise   | p               | decision limit | gene symbol |  |
| 204069_at              | 3.31118886883646  | 0*              | 482.55         | MEIS1       |  |
| 219033_at              | 3.24786485857293  | 0               |                | FLJ21308    |  |
| 219463_at              | 2.78353259146178  | 0               |                | C20orf103   |  |
| 221969_at              | 2.4416835946504   | 0               |                | PAX5        |  |
| 201874_at              | 2.38057857279198  | 0               |                | FLJ21047    |  |
| 209170_s_at            | 2.31526351178702  | 0               |                | GPM6B       |  |
| 233500_x_at            | 2.23629715560156  | 0               |                | LLT1        |  |
| 205899_at              | 2.23375311954146  | 0               |                | CCNA1       |  |
| 242414_at              | 2.21567202901383  | 0               |                |             |  |
| 205821_at              | 2.10144186601662  | 0               |                | D12S2489E   |  |
| 205055_at              | 2.04951650013049  | 0               |                | ITGAE       |  |
| 209168_at              | 2.02899949049115  | 0               |                | GPM6B       |  |
| 226939_at              | 1.99568402107224  | 0               |                |             |  |
| 209354_at              | -1.9938191217443  | 0               |                | TNFRSF14    |  |
| 200906_s_at            | 1.9632986862999   | 0               |                |             |  |
| 225563_at              | 1.88712595721941  | 0               |                |             |  |
| 237431_at              | 1.87880985981148  | 0               |                |             |  |
| 34210_at               | -1.86187594200254 | 0               |                | CDW52       |  |
| 202853_s_at            | -1.84984316383277 | 0               |                | RYK         |  |
| 209167_at              | 1.84829764568262  | 0               |                | GPM6B       |  |

## ALL t(4;11) vs. T-ALL

samples: 9 / 9

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

221969\_at

5.83664657385464

0\*

1301

PAX5

237431\_at

5.31661820706767

0

213772\_s\_at

4.80540935532116

0

GGA2

219463\_at

3.9253737114322

0

C20orf103

210934\_at

3.72127171897839

0

BLK

242292\_at

-3.53231266693437

0

226496\_at

3.49024496949904

0

244261\_at

3.40910490910101

0

205640\_at

3.04306419050975

0

ALDH3B1

219033\_at

3.03434195473282

0

FLJ21308

209168\_at

3.02932118514235

0

GPM6B

205821\_at

2.9956567374574

0

D12S2489E

235706\_at

2.99518505957364

0

CPM

225592\_at

2.98114633774562

0

NRM

225314\_at

-2.87525509857994

0

209170\_s\_at

2.832580891342

0

GPM6B

215925\_s\_at

2.79328349720245

0

204069\_at

2.67025815490556

0

MEIS1

210192\_at

2.63764031456982

0

ATP8A1

217080\_s\_at

2.60699026264913

0

HOMER-2B

ALL t(4;11) vs. AML +8

samples: 9 / 10

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 201828_x_at | -4.66708459109445 | 0* | 226.35         | CXX1        |
| 221969_at   | 3.82090922998168  | 0  |                | PAX5        |
| 244261_at   | 3.40910490910101  | 0  |                |             |
| 210024_s_at | -3.20983153576119 | 0  |                | UBE2E3      |
| 219013_at   | -3.19035252569463 | 0  |                | FLJ21634    |
| 226496_at   | 3.13934828480165  | 0  |                |             |
| 205821_at   | 3.04595286153542  | 0  |                | D12S2489E   |
| 219229_at   | -3.04273361188054 | 0  |                | SLC21A11    |
| 222422_s_at | -3.02123752629534 | 0  |                | MGC10924    |
| 233138_at   | 2.95580347805273  | 0  |                |             |
| 206255_at   | 2.76163042569406  | 0  |                | BLK         |
| 217979_at   | 2.7584725396168   | 0  |                | NET-6       |
| 203796_s_at | 2.72124988867035  | 0  |                | BCL7A       |
| 214761_at   | 2.62282117562643  | 0  |                | OAZ         |
| 227407_at   | 2.55763093921665  | 0  |                |             |
| 209365_s_at | 2.53044674597142  | 0  |                | ECM1        |
| 228379_at   | 2.52915026244479  | 0  |                |             |
| 204214_s_at | -2.51760565011465 | 0  |                | RAB32       |
| 202626_s_at | -2.5141028457265  | 0  |                | LYN         |
| 244876_at   | 2.46777854429452  | 0  |                |             |

| ALL t(4;11) vs. AML complex |                   | samples: 9 / 36 |                |             |  |
|-----------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                    | 1                 |                 |                |             |  |
| confidence                  | 1                 |                 |                |             |  |
| gene                        | signal-to-noise   | p               | decision limit | gene symbol |  |
| 221969_at                   | 4.27209531988207  | 0*              | 1815.1         | PAX5        |  |
| 210934_at                   | 3.72127171897839  | 0               |                | BLK         |  |
| 244261_at                   | 3.40910490910101  | 0               |                |             |  |
| 219463_at                   | 3.31691046444078  | 0               |                | C20orf103   |  |
| 206255_at                   | 2.78386884086495  | 0               |                | BLK         |  |
| 226496_at                   | 2.68550006340332  | 0               |                |             |  |
| 209170_s_at                 | 2.55250295984436  | 0               |                | GPM6B       |  |
| 209168_at                   | 2.44311832949527  | 0               |                | GPM6B       |  |
| 215925_s_at                 | 2.34663986373513  | 0               |                |             |  |
| 226244_at                   | 2.33002353009868  | 0               |                |             |  |
| 219033_at                   | 2.29968992798521  | 0               |                | FLJ21308    |  |
| 205821_at                   | 2.2854186259635   | 0               |                | D12S2489E   |  |
| 232201_at                   | 2.05970386931189  | 0               |                | NKD2        |  |
| 209167_at                   | 2.05931372040727  | 0               |                | GPM6B       |  |
| 244876_at                   | 2.04904743648645  | 0               |                |             |  |
| 212658_at                   | -2.00156707557967 | 0               |                | LHFPL2      |  |
| 227407_at                   | 1.9737052609863   | 0               |                |             |  |
| 202853_s_at                 | -1.93859575890205 | 0               |                | RYK         |  |
| 203796_s_at                 | 1.92961910857241  | 0               |                | BCL7A       |  |
| 214761_at                   | 1.92608972571974  | 0               |                | OAZ         |  |

| ALL t(4;11) vs. AML normal |                  | samples: 9 / 62 |                |             |  |
|----------------------------|------------------|-----------------|----------------|-------------|--|
| accuracy                   | 1                |                 |                |             |  |
| confidence                 | 1                |                 |                |             |  |
| gene                       | signal-to-noise  | p               | decision limit | gene symbol |  |
| 221969_at                  | 4.52880455396521 | 0*              | 1791.55        | PAX5        |  |
| 210934_at                  | 3.72127171897839 | 0               |                | BLK         |  |
| 205821_at                  | 2.95344549198955 | 0               |                | D12S2489E   |  |
| 206255_at                  | 2.91976312133621 | 0               |                | BLK         |  |
| 226496_at                  | 2.83306188482026 | 0               |                |             |  |
| 215925_s_at                | 2.5921353451626  | 0               |                |             |  |
| 244261_at                  | 2.54559007441965 | 0               |                |             |  |
| 244876_at                  | 2.46777854429452 | 0               |                |             |  |
| 203796_s_at                | 2.38175636157975 | 0               |                | BCL7A       |  |
| 209815_at                  | 2.31390268701643 | 0               |                | PTCH        |  |
| 204215_at                  | 2.24841200417248 | 0               |                | MGC4175     |  |
| 227407_at                  | 2.2323195471751  | 0               |                |             |  |
| 214761_at                  | 2.22867492056937 | 0               |                | OAZ         |  |
| 226244_at                  | 2.1571079710692  | 0               |                |             |  |
| 225563_at                  | 2.13989749649066 | 0               |                |             |  |
| 225592_at                  | 2.10215542418477 | 0               |                | NRM         |  |
| 35974_at                   | 2.05472986731736 | 0               |                | LRMP        |  |
| 217979_at                  | 2.03188116697557 | 0               |                | NET-6       |  |
| 230292_at                  | 2.02307533754428 | 0               |                |             |  |
| 209168_at                  | 2.01872981119451 | 0               |                | GPM6B       |  |

| ALL t(4;11)_vs. AML t(8;21) |                   | samples: 9 / 13 |                |             |  |
|-----------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                    | 1                 |                 |                |             |  |
| confidence                  | 1                 |                 |                |             |  |
| gene                        | signal-to-noise   | p               | decision limit | gene symbol |  |
| 212484_at                   | 4.34689222808594  | 0*              | 121.4          | MTVR        |  |
| 221969_at                   | 4.27496053785902  | 0               |                | PAX5        |  |
| 203796_s_at                 | 4.18407933075926  | 0               |                | BCL7A       |  |
| 219463_at                   | 3.9253737114322   | 0               |                | C20orf103   |  |
| 210934_at                   | 3.72127171897839  | 0               |                | BLK         |  |
| 232201_at                   | 3.50091671488931  | 0               |                | NKD2        |  |
| 244261_at                   | 3.40910490910101  | 0               |                |             |  |
| 204069_at                   | 3.34624733362178  | 0               |                | MEIS1       |  |
| 204214_s_at                 | -3.30583121065186 | 0               |                | RAB32       |  |
| 225592_at                   | 3.20386305207036  | 0               |                | NRM         |  |
| 206255_at                   | 3.14140321370378  | 0               |                | BLK         |  |
| 212658_at                   | -3.07377549400227 | 0               |                | LHFPL2      |  |
| 226496_at                   | 3.07152636043149  | 0               |                |             |  |
| 233138_at                   | 2.95580347805273  | 0               |                |             |  |
| 227041_at                   | 2.93637529041438  | 0               |                |             |  |
| 212480_at                   | 2.90213688157125  | 0               |                | KIAA0376    |  |
| 203795_s_at                 | 2.86560617331268  | 0               |                | BCL7A       |  |
| 202853_s_at                 | -2.76308096012904 | 0               |                | RYK         |  |
| 203949_at                   | -2.76134156327152 | 0               |                | MPO         |  |
| 219033_at                   | 2.72927502272681  | 0               |                | FLJ21308    |  |

| AML t(15;17) vs. all other |                   | samples: 20 / 249 |                |             |  |
|----------------------------|-------------------|-------------------|----------------|-------------|--|
| accuracy                   | 1                 |                   |                |             |  |
| confidence                 | 0.984095291727473 |                   |                |             |  |
| gene                       | signal-to-noise   | p                 | decision limit | gene symbol |  |
| 214450_at                  | 2.5552572465358   | 0                 |                | CTSW        |  |
| 38487_at                   | 2.48122703820417  | 0*                | 5275.3         | FLJ12442    |  |
| 212953_x_at                | 2.383904085321    | 0                 |                | CALR        |  |
| 224794_s_at                | 2.04094710734487  | 0                 |                | LOC51148    |  |
| 221004_s_at                | 2.02822882303862  | 0                 |                | ITM3        |  |
| 204150_at                  | 1.96620111034732  | 0                 |                | STAB1       |  |
| 203948_s_at                | 1.77090499793556  | 0*                | 13772.15       | MPO         |  |
| 219837_s_at                | 1.67874985207037  | 0                 |                | C17         |  |
| 205382_s_at                | 1.63444144003612  | 0                 |                | DF          |  |
| 241383_at                  | 1.6305764545467   | 0                 |                |             |  |
| 216032_s_at                | 1.61454780261863  | 0                 |                | SDBCAG84    |  |
| 200654_at                  | 1.60202170245338  | 0                 |                | P4HB        |  |
| 220798_x_at                | 1.58679638297009  | 0                 |                | FLJ11535    |  |
| 208852_s_at                | 1.58602299942644  | 0                 |                | CANX        |  |
| 203074_at                  | 1.57040201174593  | 0                 |                | ANXA8       |  |
| 200656_s_at                | 1.55688359776913  | 0                 |                | P4HB        |  |
| 209344_at                  | 1.55490125921714  | 0                 |                | TPM4        |  |
| 205624_at                  | 1.52362814764187  | 0                 |                | CPA3        |  |
| 64942_at                   | 1.52358978934783  | 0                 |                |             |  |
| AFFX-                      |                   |                   |                |             |  |
| HUMGAPDH/M33197_5_at       | -                 |                   |                |             |  |
| HG-U133A                   | 1.05449125226594  | 0                 |                | GAPD        |  |



| AML t(15;17) vs. AML inv(16) |                   | samples: 20 / 12 |                |             |  |
|------------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                     | 1                 |                  |                |             |  |
| confidence                   | 1                 |                  |                |             |  |
| gene                         | signal-to-noise   | p                | decision limit | gene symbol |  |
| 204661_at                    | -3.70847055085953 | 0*               | 1899.15        | CDW52       |  |
| 209732_at                    | -3.23538966029247 | 0                |                | CLECSF2     |  |
| 241742_at                    | -3.11768531834572 | 0                |                | PRAM-1      |  |
| 38487_at                     | 3.08138549900179  | 0                |                | FLJ12442    |  |
| 238022_at                    | 3.0278549438122   | 0                |                |             |  |
| 204563_at                    | -2.99471501611954 | 0                |                | SELL        |  |
| 34210_at                     | -2.99398735377828 | 0                |                | CDW52       |  |
| 203535_at                    | -2.97123029136408 | 0                |                | S100A9      |  |
| 217478_s_at                  | -2.93655072055469 | 0                |                |             |  |
| 214450_at                    | 2.92945546081029  | 0                |                | CTSW        |  |
| 211991_s_at                  | -2.91096104465505 | 0                |                | HLA-DPA1    |  |
| 208306_x_at                  | -2.87060964824031 | 0                |                | HLA-DRB4    |  |
| 213779_at                    | 2.84856846381654  | 0                |                |             |  |
| 211990_at                    | -2.76844422327205 | 0                |                | HLA-DPA1    |  |
| 221004_s_at                  | 2.72545702224706  | 0                |                | ITM3        |  |
| 209312_x_at                  | -2.66880572066538 | 0                |                | HLA-DRB1    |  |
| 219789_at                    | -2.64334906817191 | 0                |                | NPR3        |  |
| 204425_at                    | -2.62831954360607 | 0                |                | ARHGAP4     |  |
| 205076_s_at                  | -2.59502309617401 | 0                |                | CRA         |  |
| 64942_at                     | 2.28304127550384  | 0                |                |             |  |

|                          |                   |                  |                |             |
|--------------------------|-------------------|------------------|----------------|-------------|
| AML t(15;17) vs. AML MLL |                   | samples: 20 / 15 |                |             |
| accuracy                 | 1                 |                  |                |             |
| confidence               | 1                 |                  |                |             |
| gene                     | signal-to-noise   | p                | decision limit | gene symbol |
| 205624_at                | 3.0741697102978   | 0*               | 2052.6         | CPA3        |
| 38487_at                 | 2.78111206643545  | 0                |                | FLJ12442    |
| 203948_s_at              | 2.68497999695567  | 0                |                | MPO         |
| 221004_s_at              | 2.64526084301972  | 0                |                | ITM3        |
| 200951_s_at              | 2.52924582612911  | 0                |                | CCND2       |
| 206761_at                | 2.52586949939666  | 0                |                | TACTILE     |
| 203949_at                | 2.44678680592608  | 0                |                | MPO         |
| 214651_s_at              | -2.42192013365627 | 0                |                | HOXA9       |
| 200952_s_at              | 2.39696270141848  | 0                |                | CCND2       |
| 64942_at                 | 2.28304127550384  | 0                |                |             |
| 200953_s_at              | 2.24845652213108  | 0                |                | CCND2       |
| 204150_at                | 2.2435902165197   | 0                |                | STAB1       |
| 212953_x_at              | 2.22414089725316  | 0                |                | CALR        |
| 233072_at                | 2.22380780245302  | 0                |                | KIAA1857    |
| 214450_at                | 2.16984309325722  | 0                |                | CTSW        |
| 224794_s_at              | 2.14479331910386  | 0                |                | LOC51148    |
| 205349_at                | 2.12589700684588  | 0                |                | GNA15       |
| 212509_s_at              | 2.11142192746438  | 0                |                |             |
| 224839_s_at              | 2.07810412712239  | 0                |                | GPT2        |
| 210788_s_at              | 2.07490438621852  | 0                |                | LOC51635    |

|                             |                        |                  |                       |                    |
|-----------------------------|------------------------|------------------|-----------------------|--------------------|
| <b>AML t(15;17) vs. CLL</b> |                        | samples: 20 / 32 |                       |                    |
| accuracy                    | 1                      |                  |                       |                    |
| confidence                  | 1                      |                  |                       |                    |
| <b>gene</b>                 | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 203949_at                   | 6.8835946674069        | 0*               | 5834.85               | MPO                |
| 203948_s_at                 | 5.89121269767824       | 0                |                       | MPO                |
| 206871_at                   | 4.93321162912793       | 0                |                       | ELA2               |
| 226043_at                   | 4.54092115946342       | 0                |                       | AGS3               |
| 213854_at                   | 4.34395164475566       | 0                |                       | SYNGR1             |
| 224918_x_at                 | 4.34201320024004       | 0                |                       | MGST1              |
| 206111_at                   | 4.19970662571818       | 0                |                       | RNASE2             |
| 200654_at                   | 4.03204616783544       | 0                |                       | P4HB               |
| 231736_x_at                 | 4.00585801175558       | 0                |                       | MGST1              |
| 224838_at                   | -3.92476184954236      | 0                |                       |                    |
| 211990_at                   | -3.92005265639026      | 0                |                       | HLA-DPA1           |
| 238583_at                   | 3.81099135622948       | 0                |                       |                    |
| 221004_s_at                 | 3.79791980511322       | 0                |                       | ITM3               |
| 212400_at                   | -3.75779674692328      | 0                |                       |                    |
| 211709_s_at                 | 3.73806507086654       | 0                |                       | SCGF               |
| 214575_s_at                 | 3.66149641725929       | 0                |                       | AZU1               |
| 205382_s_at                 | 3.59180789007477       | 0                |                       | DF                 |
| 238022_at                   | 3.5791572544895        | 0                |                       |                    |
| 212953_x_at                 | 3.54883221957949       | 0                |                       | CALR               |
| 38487_at                    | 3.51682772737691       | 0                |                       | FLJ12442           |

| AML t(15;17) vs. CML |                   | samples: 20 / 14 |                |             |  |
|----------------------|-------------------|------------------|----------------|-------------|--|
| accuracy             | 1                 |                  |                |             |  |
| confidence           | 1                 |                  |                |             |  |
| gene                 | signal-to-noise   | p                | decision limit | gene symbol |  |
| 201029_s_at          | 4.80190269912041  | 0*               | 4487.95        | MIC2        |  |
| 212531_at            | -4.73996757450677 | 0                |                | LCN2        |  |
| 206676_at            | -4.32531789709243 | 0                |                | CEACAM8     |  |
| 216379_x_at          | -4.27706524116979 | 0                |                |             |  |
| 209771_x_at          | -4.21950511119586 | 0                |                | CD24        |  |
| 207269_at            | -3.91601606801308 | 0                |                | DEFA4       |  |
| 205557_at            | -3.83288724786037 | 0                |                | BPI         |  |
| 202018_s_at          | -3.78757135021052 | 0                |                | LTF         |  |
| 38487_at             | 3.67170603901023  | 0                |                | FLJ12442    |  |
| 211657_at            | -3.58933972989264 | 0                |                |             |  |
| 205382_s_at          | 3.52725281328905  | 0                |                | DF          |  |
| 220798_x_at          | 3.50808230625528  | 0                |                | FLJ11535    |  |
| 209772_s_at          | -3.45628903280328 | 0                |                | CD24        |  |
| 221004_s_at          | 3.42707462770742  | 0                |                | ITM3        |  |
| 203535_at            | -3.38406746753723 | 0                |                | S100A9      |  |
| 205863_at            | -3.37594312179774 | 0                |                | S100A12     |  |
| 204174_at            | -3.3757799683273  | 0                |                | ALOX5AP     |  |
| 203757_s_at          | -3.33946937382462 | 0                |                | CEACAM6     |  |
| 225386_s_at          | -3.31814635286046 | 0                |                | LOC92906    |  |
| 64942_at             | 2.28304127550384  | 0                |                |             |  |

| AML t(15;17) vs. normal BM |                   | samples: 20 / 9 |                |             |  |
|----------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                   | 1                 |                 |                |             |  |
| confidence                 | 1                 |                 |                |             |  |
| gene                       | signal-to-noise   | p               | decision limit | gene symbol |  |
| 225792_at                  | -5.04037264761662 | 0*              | 76.45          |             |  |
| 202018_s_at                | -5.02314565371121 | 0               |                | LTF         |  |
| 223280_x_at                | -4.43579892206636 | 0               |                | MS4A6A      |  |
| 212531_at                  | -4.09661809496392 | 0               |                | LCN2        |  |
| 203535_at                  | -3.97435355306196 | 0               |                | S100A9      |  |
| 205382_s_at                | 3.87917813251128  | 0               |                | DF          |  |
| 224356_x_at                | -3.8624083855044  | 0               |                | MS4A6A      |  |
| 201029_s_at                | 3.64114093559717  | 0               |                | MIC2        |  |
| 219471_at                  | -3.59149059254273 | 0               |                | FLJ21562    |  |
| 223391_at                  | -3.55822107244772 | 0               |                | LOC81537    |  |
| 225897_at                  | -3.53074009879907 | 0               |                |             |  |
| 209831_x_at                | 3.47754001947329  | 0               |                | DNASE2      |  |
| 230526_at                  | -3.32964763857134 | 0               |                | FLJ20015    |  |
| 221004_s_at                | 3.30073847019088  | 0               |                | ITM3        |  |
| 38487_at                   | 3.26067308155523  | 0               |                | FLJ12442    |  |
| 207697_x_at                | -3.24955398927113 | 0               |                | LILRB2      |  |
| 203645_s_at                | -3.22408073656527 | 0               |                | CD163       |  |
| 201506_at                  | -3.1496662320639  | 0               |                | TGFB1       |  |
| 239278_at                  | -3.14559842984954 | 0               |                |             |  |
| 201640_x_at                | 3.1436907617525   | 0               |                | CLPTM1      |  |

| AML t(15;17) vs. ALL t(8;14) |                   | samples: 20 / 4 |                |             |  |
|------------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                     | 1                 |                 |                |             |  |
| confidence                   | 1                 |                 |                |             |  |
| gene                         | signal-to-noise   | p               | decision limit | gene symbol |  |
| 212400_at                    | -6.34509116618667 | 0*              | 124.35         | KIAA1842    |  |
| 239835_at                    | -4.64446812677972 | 0               |                | SYNGR1      |  |
| 213854_at                    | 4.34395164475566  | 0               |                | ADAM19      |  |
| 209765_at                    | -3.90392395971701 | 0               |                | CALR        |  |
| 212953_x_at                  | 3.6338360358333   | 0               |                | FLJ11535    |  |
| 220798_x_at                  | 3.50808230625528  | 0               |                | FOXO1A      |  |
| 202723_s_at                  | -3.43565959824609 | 0               |                | DF          |  |
| 205382_s_at                  | 3.38600016039015  | 0               |                | IDUA        |  |
| 205059_s_at                  | 3.37067676532123  | 0               |                | FLJ12442    |  |
| 38487_at                     | 3.30566285802216  | 0               |                |             |  |
| 235823_at                    | -3.22388670008998 | 0               |                | CTSW        |  |
| 214450_at                    | 3.19435746487831  | 0               |                | CLPTM1      |  |
| 201640_x_at                  | 3.1436907617525   | 0               |                | SYNE-2      |  |
| 242774_at                    | -3.10884740483827 | 0               |                | CPA3        |  |
| 205624_at                    | 3.08135190030361  | 0               |                | ITM3        |  |
| 221004_s_at                  | 3.04980072799641  | 0               |                | DDAH2       |  |
| 202262_x_at                  | 3.00631284337625  | 0               |                | LOC113263   |  |
| 227525_at                    | -2.99175282480629 | 0               |                | BACH2       |  |
| 227173_s_at                  | -2.97620214103741 | 0               |                | FLJ12681    |  |
| 46142_at                     | 2.45069282884032  | 0               |                |             |  |

AML t(15;17) vs. ALL B not Ph samples: 20 / 9

|             |                        |          |                       |                    |
|-------------|------------------------|----------|-----------------------|--------------------|
| accuracy    | 1                      |          |                       |                    |
| confidence  | 1                      |          |                       |                    |
| <b>gene</b> | <b>signal-to-noise</b> | <b>p</b> | <b>decision limit</b> | <b>gene symbol</b> |
| 205382_s_at | 3.94103663553541       | 0*       | 3034.4                | DF                 |
| 214450_at   | 3.7272017152315        | 0        |                       | CTSW               |
| 220798_x_at | 3.50808230625528       | 0        |                       | FLJ11535           |
| 209831_x_at | 3.47754001947329       | 0        |                       | DNASE2             |
| 212953_x_at | 3.01141919123014       | 0        |                       | CALR               |
| 231736_x_at | 2.98271279100376       | 0        |                       | MGST1              |
| 211990_at   | -2.92818453065756      | 0        |                       | HLA-DPA1           |
| 241383_at   | 2.90001109867359       | 0        |                       |                    |
| 224918_x_at | 2.89999004151056       | 0        |                       | MGST1              |
| 205624_at   | 2.84403833450845       | 0        |                       | CPA3               |
| 38487_at    | 2.72794873611638       | 0        |                       | FLJ12442           |
| 200654_at   | 2.71316195189784       | 0        |                       | P4HB               |
| 221004_s_at | 2.68426024071363       | 0        |                       | ITM3               |
| 208689_s_at | 2.62363368134519       | 0        |                       | RPN2               |
| 221739_at   | 2.61870113363546       | 0        |                       | IL27               |
| 203679_at   | 2.54794444503946       | 0        |                       | IL1RL1LG           |
| 217716_s_at | 2.27011720191064       | 0        |                       | SEC61A1            |
| 208852_s_at | 2.24073987327423       | 0        |                       | CANX               |
| 220744_s_at | 2.21509524546031       | 0        |                       | WDR10              |
| 55093_at    | 1.63667373135171       | 0        |                       | KIAA1402           |

| AML t(15;17) vs. ALL Ph |                   | samples: 20 / 15 |                |             |  |
|-------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                | 1                 |                  |                |             |  |
| confidence              | 1                 |                  |                |             |  |
| gene                    | signal-to-noise   | p                | decision limit | gene symbol |  |
| 211990_at               | -3.8327925790289  | 0                | 41             | HLA-DPA1    |  |
| 220798_x_at             | 3.50808230625528  | 0*               |                | FLJ11535    |  |
| 224918_x_at             | 3.50754573671859  | 0                |                | MGST1       |  |
| 214450_at               | 3.50155234311803  | 0                |                | CTSW        |  |
| 231736_x_at             | 3.3802502122888   | 0                |                | MGST1       |  |
| 205624_at               | 3.21024990481945  | 0                |                | CPA3        |  |
| 203373_at               | -3.1946557461653  | 0                |                | STAT2       |  |
| 205382_s_at             | 3.14485336319038  | 0                |                | DF          |  |
| 212953_x_at             | 2.86696122083705  | 0                |                | CALR        |  |
| 203948_s_at             | 2.80859584810434  | 0                |                | MPO         |  |
| 238583_at               | 2.78542343697266  | 0                |                |             |  |
| 209732_at               | -2.73475243434259 | 0                |                | CLECSF2     |  |
| 233072_at               | 2.63743334734262  | 0                |                | KIAA1857    |  |
| 209619_at               | -2.55642326842901 | 0                |                | CD74        |  |
| 226545_at               | -2.50061887472005 | 0                |                |             |  |
| 238022_at               | 2.48587783472615  | 0                |                |             |  |
| 210487_at               | -2.48460923232205 | 0                |                | DNTT        |  |
| 200654_at               | 2.41521499865532  | 0                |                | P4HB        |  |
| 209831_x_at             | 2.34522293184427  | 0                |                | DNASE2      |  |
| 225790_at               | 2.31674527318944  | 0                |                |             |  |



## AML t(15;17) vs. T-ALL

samples: 20 / 9

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 203949_at   | 5.76493681986315  | 0* | 6205           | MPO         |
| 203948_s_at | 5.52731611865475  | 0  |                | MPO         |
| 224918_x_at | 5.05683576581082  | 0  |                | MGST1       |
| 231736_x_at | 4.44324813542895  | 0  |                | MGST1       |
| 213854_at   | 4.34395164475566  | 0  |                | SYNGR1      |
| 205382_s_at | 4.13724322163424  | 0  |                | DF          |
| 206871_at   | 4.09729897232645  | 0  |                | ELA2        |
| 206111_at   | 3.61313451786675  | 0  |                | RNASE2      |
| 242292_at   | -3.53231266693437 | 0  |                |             |
| 214575_s_at | 3.51522052980985  | 0  |                | AZU1        |
| 220798_x_at | 3.50808230625528  | 0  |                | FLJ11535    |
| 38487_at    | 3.40780715783254  | 0  |                | FLJ12442    |
| 200654_at   | 3.36034425167829  | 0  |                | P4HB        |
| 235101_at   | -3.27592263847035 | 0  |                | KIAA1014    |
| 208689_s_at | 3.18547214467073  | 0  |                | RPN2        |
| 212953_x_at | 3.18316032369792  | 0  |                | CALR        |
| 204348_s_at | 3.06277487805438  | 0  |                | AK3         |
| 201537_s_at | 2.82382291089523  | 0  |                | DUSP3       |
| 214450_at   | 2.81907045269144  | 0  |                | CTSW        |
| 204150_at   | 2.73329912927614  | 0  |                | STAB1       |

| AML t(15;17) vs. AML +8 |                   | samples: 20 / 10 |                |             |  |
|-------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                | 1                 |                  |                |             |  |
| confidence              | 1                 |                  |                |             |  |
| gene                    | signal-to-noise   | p                | decision limit | gene symbol |  |
| 214450_at               | 3.0865086945171   | 0*               | 1926.7         | CTSW        |  |
| 212953_x_at             | 2.71319553382926  | 0                |                | CALR        |  |
| 236787_at               | 2.4273500798775   | 0                |                |             |  |
| 200952_s_at             | 2.39696270141848  | 0                |                | CCND2       |  |
| 205624_at               | 2.38480346275743  | 0                |                | CPA3        |  |
| 38487_at                | 2.38251622694176  | 0                |                | FLJ12442    |  |
| 205614_x_at             | 2.24846130719191  | 0                |                | MST1        |  |
| 206761_at               | 2.20501899975366  | 0                |                | TACTILE     |  |
| 216320_x_at             | 2.16690689445934  | 0                |                |             |  |
| 224794_s_at             | 2.14479331910386  | 0                |                | LOC51148    |  |
| 233072_at               | 2.07721746169547  | 0                |                | KIAA1857    |  |
| 221004_s_at             | 2.05892662897696  | 0                |                | ITM3        |  |
| 227326_at               | 2.04924504239987  | 0                |                |             |  |
| 221980_at               | 2.01752809990056  | 0                |                |             |  |
| 225547_at               | -1.98126007880124 | 0                |                |             |  |
| 210145_at               | -1.95455412087558 | 0                |                | PLA2G4A     |  |
| 212509_s_at             | 1.92046303571342  | 0                |                |             |  |
| 209344_at               | 1.90906303754685  | 0                |                | TPM4        |  |
| 201029_s_at             | 1.87538506046111  | 0                |                | MIC2        |  |
| 204150_at               | 1.87343002266891  | 0                |                | STAB1       |  |

AML t(15;17) vs. AML

complex samples: 20 / 36

accuracy 1

confidence 1

| gene                 | signal-to-noise   | p  | decision limit | gene symbol |
|----------------------|-------------------|----|----------------|-------------|
| 205382_s_at          | 2.47024872277389  | 0  |                | DF          |
| 212953_x_at          | 2.44599456599903  | 0* | 4652.35        | CALR        |
| 64942_at             | 2.28304127550384  | 0  |                |             |
| 214450_at            | 2.2627370518124   | 0  |                | CTSW        |
| 38487_at             | 2.15395063071356  | 0  |                | FLJ12442    |
| 224794_s_at          | 2.14479331910386  | 0  |                | LOC51148    |
| 220798_x_at          | 2.06303065394458  | 0  |                | FLJ11535    |
| 216032_s_at          | 2.05259440043708  | 0  |                | SDBCAG84    |
| 203948_s_at          | 2.04245448483567  | 0  |                | MPO         |
| 209732_at            | -1.90630142681759 | 0  |                | CLECSF2     |
| 230526_at            | -1.90204644112897 | 0  |                | FLJ20015    |
| 238022_at            | 1.89121106100583  | 0  |                |             |
| 200654_at            | 1.73209407132843  | 0  |                | P4HB        |
| 204150_at            | 1.72000809746397  | 0  |                | STAB1       |
| 213447_at            | -1.71480861978241 | 0  |                | IPW         |
| 206847_s_at          | -1.68023930751716 | 0  |                | HOXA7       |
| 203074_at            | 1.65576107663154  | 0  |                | ANXA8       |
| 219837_s_at          | 1.65191807395586  | 0  |                | C17         |
| 200931_s_at          | -1.6356222023809  | 0  |                | VCL         |
| AFFX-                |                   |    |                |             |
| HUMGAPDH/M33197_5_at | -                 |    |                |             |
| HG-U133A             | 1.15678566237816  | 0  |                | GAPD        |

| AML t(15;17) vs. AML normal |                   | samples: 20 / 62 |                |             |  |
|-----------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                    | 1                 |                  |                |             |  |
| confidence                  | 1                 |                  |                |             |  |
| gene                        | signal-to-noise   | p                | decision limit | gene symbol |  |
| 212953_x_at                 | 2.64618373092816  | 0*               | 4541.1         | CALR        |  |
| 214450_at                   | 2.28653040002124  | 0                |                | CTSW        |  |
| 203948_s_at                 | 2.28093863578688  | 0                |                | MPO         |  |
| 38487_at                    | 2.27897339525457  | 0                |                | FLJ12442    |  |
| 224794_s_at                 | 2.14479331910386  | 0                |                | LOC51148    |  |
| 233072_at                   | 2.02319157581908  | 0                |                | KIAA1857    |  |
| 221004_s_at                 | 2.01169552990941  | 0                |                | ITM3        |  |
| 236787_at                   | 1.97410536661333  | 0                |                |             |  |
| 209732_at                   | -1.93278822451406 | 0                |                | CLECSF2     |  |
| 214651_s_at                 | -1.88045707977072 | 0                |                | HOXA9       |  |
| 216032_s_at                 | 1.84310066944834  | 0                |                | SDBCAG84    |  |
| 227326_at                   | 1.83154138034996  | 0                |                |             |  |
| 200952_s_at                 | 1.79422847402715  | 0                |                | CCND2       |  |
| 208852_s_at                 | 1.77896258332914  | 0                |                | CANX        |  |
| 200654_at                   | 1.77731955574697  | 0                |                | P4HB        |  |
| 204150_at                   | 1.77067560905128  | 0                |                | STAB1       |  |
| 64942_at                    | 1.71976456537364  | 0                |                |             |  |
| 203949_at                   | 1.69386661503752  | 0                |                | MPO         |  |
| 235753_at                   | -1.67072227461966 | 0                |                |             |  |
| 209344_at                   | 1.65496211687573  | 0                |                | TPM4        |  |

| AML t(15;17) vs. AML t(8;21) |                   | samples: 20 / 13 |                |             |  |
|------------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                     | 1                 |                  |                |             |  |
| confidence                   | 1                 |                  |                |             |  |
| gene                         | signal-to-noise   | p                | decision limit | gene symbol |  |
| 214450_at                    | 3.53862069365814  | 0*               | 1809.95        | CTSW        |  |
| 38487_at                     | 3.30334484935728  | 0                |                | FLJ12442    |  |
| 209732_at                    | -3.18277220746091 | 0                |                | CLECSF2     |  |
| 204150_at                    | 2.73329912927614  | 0                |                | STAB1       |  |
| 201596_x_at                  | 2.73162867034962  | 0                |                | KRT18       |  |
| 213944_x_at                  | 2.5862372690463   | 0                |                |             |  |
| 230526_at                    | -2.42276930706474 | 0                |                | FLJ20015    |  |
| 212509_s_at                  | 2.33481477262277  | 0                |                |             |  |
| 211990_at                    | -2.3270695509372  | 0                |                | HLA-DPA1    |  |
| 204319_s_at                  | -2.25060861801642 | 0                |                | RGS10       |  |
| 205614_x_at                  | 2.24846130719191  | 0                |                | MST1        |  |
| 216320_x_at                  | 2.16690689445934  | 0                |                |             |  |
| 224794_s_at                  | 2.14479331910386  | 0                |                | LOC51148    |  |
| 224839_s_at                  | 2.07810412712239  | 0                |                | GPT2        |  |
| 227326_at                    | 2.04924504239987  | 0                |                |             |  |
| 238365_s_at                  | 2.03674279873081  | 0                |                |             |  |
| 228827_at                    | -2.03460798747208 | 0                |                |             |  |
| 228570_at                    | 2.03169244854036  | 0                |                |             |  |
| 205349_at                    | 2.02142471684528  | 0                |                | GNA15       |  |
| 200986_at                    | 2.01484061650733  | 0                |                | SERPING1    |  |

|                           |                   |                   |                |             |  |
|---------------------------|-------------------|-------------------|----------------|-------------|--|
| AML inv(16) vs. all other |                   | samples: 12 / 257 |                |             |  |
| accuracy                  | 1                 |                   |                |             |  |
| confidence                | 0.786321619312236 |                   |                |             |  |
| gene                      | signal-to-noise   | p                 | decision limit | gene symbol |  |
| 201497_x_at               | 1.74852845185764  | 0                 |                | MYH11       |  |
| 231310_at                 | 1.47164364462932  | 0                 |                |             |  |
| 241525_at                 | 1.40464277333052  | 0                 |                |             |  |
| 233555_s_at               | 1.36141951191384  | 0*                | 462.05         |             |  |
| 224724_at                 | 1.35707926936144  | 0                 |                | KIAA1247    |  |
| 200665_s_at               | 1.34209700274375  | 0                 |                | SPARC       |  |
| 202370_s_at               | -1.29245470192814 | 0                 |                | CBFB        |  |
| 222862_s_at               | 1.26048366428059  | 0                 |                | AK5         |  |
| 200675_at                 | -1.23914248971997 | 0                 |                | CD81        |  |
| 205076_s_at               | 1.22017942852008  | 0                 |                | CRA         |  |
| 201496_x_at               | 1.21510481759962  | 0                 |                | MYH11       |  |
| 223385_at                 | 1.2113380867898   | 0                 |                | CYP2S1      |  |
| 221486_at                 | -1.19152063013451 | 0                 |                |             |  |
| 223471_at                 | -1.18312106893472 | 0                 |                |             |  |
| 206135_at                 | 1.18181935093584  | 0                 |                | KIAA0535    |  |
| 206956_at                 | 1.17922310970084  | 0                 |                | BGLAP       |  |
| 235359_at                 | 1.16409001423194  | 0                 |                |             |  |
| 202016_at                 | 1.15872909212242  | 0*                | 1              | MEST        |  |
| 201324_at                 | 1.15017496156271  | 0                 |                | EMP1        |  |
| AFFX-HUMRGE/M10098_5_at   |                   |                   |                |             |  |
| - HG-U133B                | 0.737113176900438 | 0                 |                |             |  |

| AML inv(16) vs. AML MLL |                   | samples: 12 / 15 |                |             |  |
|-------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                | 1                 |                  |                |             |  |
| confidence              | 1                 |                  |                |             |  |
| gene                    | signal-to-noise   | p                | decision limit | gene symbol |  |
| 200951_s_at             | 4.24994685464806  | 0*               | 75.6           | CCND2       |  |
| 228058_at               | 3.25212044058077  | 0                |                |             |  |
| 219271_at               | 2.57049778814556  | 0                |                | FLJ12691    |  |
| 231259_s_at             | 2.43255056573718  | 0                |                | CCND2       |  |
| 214651_s_at             | -2.30388406553935 | 0                |                | HOXA9       |  |
| 202551_s_at             | 2.25890379783091  | 0                |                | CRIM1       |  |
| 205453_at               | 2.23059959679219  | 0                |                | HOXB2       |  |
| 200953_s_at             | 2.19700687874039  | 0                |                | CCND2       |  |
| 213737_x_at             | -2.16186095833837 | 0                |                |             |  |
| 235818_at               | 2.13054793207832  | 0                |                |             |  |
| 225653_at               | 2.10834669134201  | 0                |                |             |  |
| 232636_at               | -2.07022186491858 | 0                |                |             |  |
| 202746_at               | 2.06211630393441  | 0                |                |             |  |
| 200665_s_at             | 2.03751489015447  | 0                |                | SPARC       |  |
| 203949_at               | 2.01364277991339  | 0                |                | MPO         |  |
| 202552_s_at             | 1.96670486082105  | 0                |                | CRIM1       |  |
| 223471_at               | -1.96529988161274 | 0                |                |             |  |
| 201828_x_at             | -1.9593150488894  | 0                |                | CXX1        |  |
| 235359_at               | 1.95403665761428  | 0                |                |             |  |
| 202747_s_at             | 1.9384101680124   | 0                |                | ITM2A       |  |

## AML inv(16) vs. CLL

samples: 12 / 32

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 203949_at   | 6.95021247410033  | 0* | 3746.5         | MPO         |
| 211709_s_at | 5.18681505358433  | 0  |                | SCGF        |
| 203948_s_at | 4.72760268663435  | 0  |                | MPO         |
| 231310_at   | 4.35158499850242  | 0  |                |             |
| 226043_at   | 4.31805631251135  | 0  |                | AGS3        |
| 201417_at   | 3.83165504179581  | 0  |                |             |
| 209365_s_at | 3.8293529362527   | 0  |                | ECM1        |
| 224838_at   | -3.72164043642693 | 0  |                |             |
| 243000_at   | 3.63182045730937  | 0  |                |             |
| 223382_s_at | 3.56679694464951  | 0  |                | NIN283      |
| 201163_s_at | 3.21223463217947  | 0  |                | IGFBP7      |
| 202862_at   | 3.20454480816595  | 0  |                | FAH         |
| 231982_at   | 3.1934694742924   | 0  |                |             |
| 201162_at   | 3.15702502490111  | 0  |                | IGFBP7      |
| 218942_at   | -3.1335063798458  | 0  |                | FLJ22055    |
| 212827_at   | -3.11017349120191 | 0  |                | IGHM        |
| 224710_at   | 3.04332806808412  | 0  |                | RAB34       |
| 208864_s_at | 3.01671716600197  | 0  |                | TXN         |
| 211787_s_at | 2.90916234544607  | 0  |                | EIF4A1      |
| 205382_s_at | 2.90564641349051  | 0  |                | DF          |



| AML inv(16).vs. CML |                   | samples: 12 / 14 |                |             |
|---------------------|-------------------|------------------|----------------|-------------|
| accuracy            | 1                 |                  |                |             |
| confidence          | 1                 |                  |                |             |
| gene                | signal-to-noise   | p                | decision limit | gene symbol |
| 201029_s_at         | 4.31890554977499  | 0*               | 4017           | MIC2        |
| 209365_s_at         | 3.8293529362527   | 0                |                | ECM1        |
| 226844_at           | 3.75460881300519  | 0                |                |             |
| 209771_x_at         | -3.55889840129944 | 0                |                | CD24        |
| 206440_at           | -3.54851691296324 | 0                |                | VEL1        |
| 233138_at           | 3.4735123827114   | 0                |                |             |
| 216379_x_at         | -3.43948341863688 | 0                |                |             |
| 227749_at           | 3.41648620394084  | 0                |                |             |
| 209772_s_at         | -3.3477199485593  | 0                |                | CD24        |
| 210982_s_at         | 3.24778523856649  | 0                |                | HLA-DRA     |
| 218942_at           | -3.24708603988632 | 0                |                | FLJ22055    |
| 206676_at           | -3.24497920147189 | 0                |                | CEACAM8     |
| 204661_at           | 3.10482803895821  | 0                |                | CDW52       |
| 212531_at           | -3.09841450182506 | 0                |                | LCN2        |
| 208306_x_at         | 3.05465357697194  | 0                |                | HLA-DRB4    |
| 208890_s_at         | 2.99789197915585  | 0                |                | PLXNB2      |
| 216015_s_at         | 2.9548034027314   | 0                |                |             |
| 223839_s_at         | -2.95162251991881 | 0                |                |             |
| 207802_at           | -2.93213346323135 | 0                |                | SGP28       |
| 34210_at            | 2.86220111493221  | 0                |                | CDW52       |

|                                  |                        |                 |                       |                    |
|----------------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>AML inv(16) vs. normal BM</b> |                        | samples: 12 / 9 |                       |                    |
| accuracy                         | 1                      |                 |                       |                    |
| confidence                       | 1                      |                 |                       |                    |
| <b>gene</b>                      | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 225792_at                        | -5.04037264761662      | 0*              | 76.45                 |                    |
| 224975_at                        | -5.01918026903577      | 0               |                       | NFIA               |
| 224976_at                        | -4.534006778733        | 0               |                       | NFIA               |
| 238652_at                        | 4.21116590562832       | 0               |                       |                    |
| 209365_s_at                      | 3.8293529362527        | 0               |                       | ECM1               |
| 223044_at                        | -3.73370982362517      | 0               |                       | SLC11A3            |
| 226326_at                        | -3.6960030140107       | 0               |                       |                    |
| 200832_s_at                      | -3.67575949264708      | 0               |                       | SCD.               |
| 213288_at                        | -3.55635098156803      | 0               |                       |                    |
| 230988_at                        | -3.46948918999612      | 0               |                       |                    |
| 205382_s_at                      | 3.29073930292859       | 0               |                       | DF                 |
| 201417_at                        | 3.27682718704937       | 0               |                       |                    |
| 225897_at                        | -3.21286424500781      | 0               |                       |                    |
| 226299_at                        | 3.21097313269574       | 0               |                       | pknbeta            |
| 210933_s_at                      | 3.17596755096177       | 0               |                       | MGC4655            |
| 218094_s_at                      | 3.1307319856851        | 0               |                       | C20orf35           |
| 201029_s_at                      | 3.10235325372561       | 0               |                       | MIC2               |
| 210036_s_at                      | -3.09612221936927      | 0               |                       | KCNH2              |
| 212667_at                        | 3.07883651171274       | 0               |                       | SPARC              |
| 40189_at                         | 2.32056421839438       | 0               |                       | SET                |

| AML inv(16) vs. ALL t(8;14) |                   | samples: 12 / 4 |                |             |  |
|-----------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                    | 1                 |                 |                |             |  |
| confidence                  | 1                 |                 |                |             |  |
| gene                        | signal-to-noise   | p               | decision limit | gene symbol |  |
| 214558_at                   | 5.11198812058407  | 0*              | 75.15          | GPR12       |  |
| 227525_at                   | -4.9287188464128  | 0               |                | LOC113263   |  |
| 211852_s_at                 | 4.75980688856888  | 0               |                | ATRN        |  |
| 238652_at                   | 4.21116590562832  | 0               |                |             |  |
| 206090_s_at                 | 4.11779253006199  | 0               |                | DISC1       |  |
| 237864_at                   | 3.94349147195948  | 0               |                |             |  |
| 225051_at                   | -3.89930170229982 | 0               |                |             |  |
| 209365_s_at                 | 3.8293529362527   | 0               |                | ECM1        |  |
| 223382_s_at                 | 3.56679694464951  | 0               |                | NIN283      |  |
| 201278_at                   | 3.38592358815787  | 0               |                | DAB2        |  |
| 219654_at                   | 3.25519407914616  | 0               |                | PTPLA       |  |
| 202074_s_at                 | -3.24311911278957 | 0               |                | OPTN        |  |
| 231982_at                   | 3.1934694742924   | 0               |                |             |  |
| 231310_at                   | 3.18344789439715  | 0               |                |             |  |
| 210933_s_at                 | 3.17596755096177  | 0               |                | MGC4655     |  |
| 222062_at                   | 3.12204176758762  | 0               |                | WSX1        |  |
| 242774_at                   | -3.10884740483827 | 0               |                | SYNE-2      |  |
| 244257_at                   | 3.09069018899455  | 0               |                |             |  |
| 212667_at                   | 3.07883651171274  | 0               |                | SPARC       |  |
| 225305_at                   | 2.99842864962803  | 0               |                |             |  |

AML inv(16) vs. ALL B not Ph samples: 12 / 9

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 205382_s_at | 3.44559828536398  | 0* | 2092.2         | DF          |
| 206772_at   | 3.36924689882826  | 0  |                | PTHR2       |
| 228058_at   | 3.25212044058077  | 0  |                |             |
| 218094_s_at | 3.1307319856851   | 0  |                | C20orf35    |
| 223385_at   | 3.07706676910952  | 0  |                | CYP2S1      |
| 204858_s_at | 2.96720397750981  | 0  |                | ECGF1       |
| 227556_at   | 2.66258700650327  | 0  |                | ATP1B1      |
| 212463_at   | -2.65372355495687 | 0  |                |             |
| 201360_at   | 2.63414688358486  | 0  |                | CST3        |
| 205997_at   | 2.6308573171159   | 0  |                | ADAM28      |
| 231310_at   | 2.60181313279404  | 0  |                |             |
| 203973_s_at | 2.4714469340582   | 0  |                | CEBPD       |
| 200872_at   | 2.42523459110761  | 0  |                | S100A10     |
| 200661_at   | 2.42407433324859  | 0  |                | PPGB        |
| 227415_at   | -2.35663515228965 | 0  |                |             |
| 219358_s_at | 2.31004642323513  | 0  |                | CENTA2      |
| 202016_at   | 2.30727907426241  | 0  |                | MEST        |
| 208248_x_at | 2.27797183411701  | 0  |                | APLP2       |
| 212188_at   | 2.26974263089413  | 0  |                | LOC115207   |
| 205076_s_at | 2.257959447417    | 0  |                | CRA         |

AML inv(16) vs. ALL Ph

samples: 12 / 15

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

231310\_at

3.26954611223081

0\*

119.2

STAT12

203373\_at

-3.07194642697668

0

DNTT

210487\_at

-2.57922739606335

0

ABCG2

209735\_at

-2.57442202182339

0

MGC11352

223314\_at

-2.46037319479876

0

TEM7R

227276\_at

2.31171718422321

0

DF

205382\_s\_at

2.30057319708762

0

S100A10

200872\_at

2.27656979916265

0

CD59

200985\_s\_at

-2.25258857041194

0

SIGLEC7

207224\_s\_at

2.24976284058658

0

APLP2

208702\_x\_at

2.21820176325777

0

CYP2E

209975\_at

2.21237181448127

0

LOC64174

219452\_at

2.18614057488219

0

MGST1

224918\_x\_at

2.18042008960618

0

PPGB

200661\_at

2.15820911658542

0

CRA

205076\_s\_at

2.1576215121228

0

TIMM44

203092\_at

-2.1346943506478

0

NET-6

217979\_at

-2.13131555913964

0

PIG3

228058\_at

2.11586185512013

0

210609\_s\_at

2.1104858897821

0

## AML inv(16) vs. T-ALL

samples: 12 / 9

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

203949\_at

5.55902965521097

0\*

4116.65

MPO

205640\_at

4.30508511818292

0

ALDH3B1

203948\_s\_at

4.299250186967

0

MPO

204484\_at

-3.92079658637056

0

PIK3C2B

223482\_at

3.8867405806948

0

TMPIT

205382\_s\_at

3.78294993092265

0

DF

242292\_at

-3.53231266693437

0

224918\_x\_at

3.39770561886615

0

MGST1

228058\_at

3.25212044058077

0

210314\_x\_at

3.15624540914219

0

TNFSF13

216015\_s\_at

2.9548034027314

0

206380\_s\_at

2.92913137540268

0

PFC

202944\_at

2.90807873450708

0

NAGA

231736\_x\_at

2.90529949191742

0

MGST1

209500\_x\_at

2.88541455460133

0

TNFSF13

205312\_at

2.86437379660673

0

SPI1

211495\_x\_at

2.85808523976773

0

TNFSF13

211101\_x\_at

2.82479786118477

0

LILRA2

219763\_at

2.71839322196283

0

KIAA1608

225510\_at

2.68685955542078

0

CHN1

AML inv(16) vs. AML +8

samples: 12 / 10

accuracy

1

confidence

1

| gene                   | signal-to-noise   | p  | decision limit | gene symbol |
|------------------------|-------------------|----|----------------|-------------|
| 233138_at              | 3.4735123827114   | 0* | 54.25          |             |
| 209365_s_at            | 3.00986865470169  | 0  |                | ECM1        |
| 202283_at              | 2.6160707896185   | 0  |                | SERPINF1    |
| 218942_at              | -2.45751904192227 | 0  |                | FLJ22055    |
| 201828_x_at            | -2.21365274281998 | 0  |                | CXX1        |
| 200951_s_at            | 2.02357943949022  | 0  |                | CCND2       |
| 226120_at              | -2.01082485261142 | 0  |                | LOC123016   |
| 203188_at              | -1.9379696222037  | 0  |                | B3GNT6      |
| 202085_at              | -1.9147903697218  | 0  |                | TJP2        |
| 206135_at              | 1.90877055638373  | 0  |                | KIAA0535    |
| 210024_s_at            | -1.90335978018863 | 0  |                | UBE2E3      |
| 204661_at              | 1.83776082826379  | 0  |                | CDW52       |
| 241525_at              | 1.83006374766269  | 0  |                |             |
| 208710_s_at            | -1.80896001968559 | 0  |                | AP3D1       |
| 34210_at               | 1.75572696362264  | 0  |                | CDW52       |
| 201497_x_at            | 1.74852845185764  | 0  |                | MYH11       |
| 212236_x_at            | 1.74679406476776  | 0  |                |             |
| 213810_s_at            | 1.69077455623534  | 0  |                | FLJ10342    |
| 212250_at              | -1.62885302351785 | 0  |                |             |
| AFFX-r2-Hs18SrRNA-5_at | -                 |    |                |             |
| HG-U133A               | 1.32018767826727  | 0  |                |             |

AML inv(16) vs. AML complex samples: 12 / 36

accuracy 1

confidence 0.957308305034528

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 203092_at   | -1.77664454556306 | 0  |                | TIMM44      |
| 209190_s_at | 1.75723541848141  | 0* | 1593.8         | DIAPH1      |
| 201497_x_at | 1.74852845185764  | 0* | 134.75         | MYH11       |
| 205076_s_at | 1.73951655525411  | 0  |                | CRA         |
| 241525_at   | 1.71682483225979  | 0  |                |             |
| 213779_at   | -1.71354352282537 | 0  |                |             |
| 210982_s_at | 1.70318998731519  | 0  |                | HLA-DRA     |
| 200985_s_at | -1.64643993864436 | 0  |                | CD59        |
| 212463_at   | -1.6457941052799  | 0  |                |             |
| 200675_at   | -1.61546783522649 | 0* | 707.85         | CD81        |
| 218942_at   | -1.59347299102441 | 0  |                | FLJ22055    |
| 200984_s_at | -1.56833724351535 | 0  |                | CD59        |
| 208894_at   | 1.54975491884609  | 0  |                | HLA-DRA     |
| 202265_at   | -1.53139324627965 | 0  |                | BMI1        |
| 224724_at   | 1.5143785002027   | 0  |                | KIAA1247    |
| 210715_s_at | -1.49004107536748 | 0  |                | SPINT2      |
| 213452_at   | -1.48522101377482 | 0  |                | ZNF184      |
| 205382_s_at | 1.45942422076027  | 0  |                | DF          |
| 201360_at   | 1.45905524413008  | 0  |                | CST3        |
| 206135_at   | 1.45729112913321  | 0  |                | KIAA0535    |



| AML inv(16) vs. AML normal |                   | samples: 12 / 62 |                |             |  |
|----------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                   | 1                 |                  |                |             |  |
| confidence                 | 0.952958978230212 |                  |                |             |  |
| gene                       | signal-to-noise   | p                | decision limit | gene symbol |  |
| 200951_s_at                | 1.82916486676122  | 0                |                | CCND2       |  |
| 209365_s_at                | 1.79092214915991  | 0*               | 390.9          | ECM1        |  |
| 214651_s_at                | -1.77796050968374 | 0*               | 187.6          | HOXA9       |  |
| 201497_x_at                | 1.74852845185764  | 0                |                | MYH11       |  |
| 231310_at                  | 1.62450567760929  | 0*               | 167.8          |             |  |
| 223385_at                  | 1.57142154491015  | 0                |                | CYP2S1      |  |
| 206135_at                  | 1.54931600211688  | 0                |                | KIAA0535    |  |
| 235753_at                  | -1.54691446076282 | 0                |                |             |  |
| 231259_s_at                | 1.52681305174601  | 0                |                | CCND2       |  |
| 204661_at                  | 1.46205490369508  | 0                |                | CDW52       |  |
| 202370_s_at                | -1.45859936190513 | 0                |                | CBFB        |  |
| 213353_at                  | -1.44758735114725 | 0                |                | ABCA5       |  |
| 209905_at                  | -1.42239381454703 | 0                |                | HOXA9       |  |
| 200675_at                  | -1.38662888859944 | 0                |                | CD81        |  |
| 207194_s_at                | 1.38591797740996  | 0                |                | ICAM4       |  |
| 201324_at                  | 1.36182933080382  | 0                |                | EMP1        |  |
| 235818_at                  | 1.35992709972839  | 0                |                |             |  |
| 225510_at                  | 1.35514122232308  | 0                |                | CHN1        |  |
| 228834_at                  | 1.35066870620531  | 0                |                | TOB1        |  |
| 34210_at                   | 1.33546826742244  | 0                |                | CDW52       |  |

| AML inv(16) vs. AML t(8;21) |                  | samples: 12 / 13 |                |             |  |
|-----------------------------|------------------|------------------|----------------|-------------|--|
| accuracy                    | 1                |                  |                |             |  |
| confidence                  | 1                |                  |                |             |  |
| gene                        | signal-to-noise  | p                | decision limit | gene symbol |  |
| 233138_at                   | 3.4735123827114  | 0*               | 54.25          |             |  |
| 202283_at                   | 2.6160707896185  | 0                |                | SERPINF1    |  |
| 201596_x_at                 | 2.55517188589615 | 0                |                | KRT18       |  |
| 233555_s_at                 | 2.48943541958708 | 0                |                |             |  |
| 226818_at                   | 2.3621676751726  | 0                |                |             |  |
| 212828_at                   | 2.33130605042964 | 0                |                | SYNJ2       |  |
| 227276_at                   | 2.31171718422321 | 0                |                | TEM7R       |  |
| 224724_at                   | 2.30850265580909 | 0                |                | KIAA1247    |  |
| 224764_at                   | 2.25934489179779 | 0                |                | ARHGAP10    |  |
| 224049_at                   | 2.25244855640038 | 0                |                | KCNK17      |  |
| 205453_at                   | 2.23059959679219 | 0                |                | HOXB2       |  |
| 226841_at                   | 2.21329419316194 | 0                |                |             |  |
| 209975_at                   | 2.21237181448127 | 0                |                | CYP2E       |  |
| 205076_s_at                 | 2.21083117233863 | 0                |                | CRA         |  |
| 202340_x_at                 | 2.18671963481275 | 0                |                | NR4A1       |  |
| 210314_x_at                 | 2.17138407196792 | 0                |                | TNFSF13     |  |
| 34689_at                    | 2.16463995293403 | 0                |                | TREX1       |  |
| 235359_at                   | 2.12423469465025 | 0                |                |             |  |
| 212188_at                   | 2.11590883979512 | 0                |                | LOC115207   |  |
| 205718_at                   | 2.10547132123535 | 0                |                | ITGB7       |  |

## AML MLL vs. all other

samples: 15 / 254

accuracy 0.977695167286245

confidence 0.736329320600874

failed: 3,6,7,11,155,212

| gene        | signal-to-noise    | p  | decision limit | gene symbol |
|-------------|--------------------|----|----------------|-------------|
| 228083_at   | 1.21941234348391   | 0  |                |             |
| 201105_at   | 1.20839678060713   | 0* | 8795.05        | LGALS1      |
| 205849_s_at | 1.03753805567643   | 0  |                | UQCRB       |
| 205472_s_at | 1.03076838857205   | 0  |                | DACH        |
| 208702_x_at | 1.01256627546813   | 0  |                | APLP2       |
| 225700_at   | -1.01092153300039  | 0  |                |             |
| 222982_x_at | -1.00741126543277  | 0* | 1101           | SLC38A2     |
| 238856_s_at | -0.990415633837559 | 0* | 1              |             |
| 214875_x_at | 0.989164186017564  | 0  |                | APLP2       |
| 209616_s_at | 0.966839890517189  | 0  |                | CES1        |
| 205471_s_at | 0.957394713027089  | 0  |                | DACH        |
| 211404_s_at | 0.942572231076861  | 0  |                | APLP2       |
| 213857_s_at | -0.933745825960995 | 0  |                | CD47        |
| 204951_at   | -0.925961455918277 | 0  |                | ARHH        |
| 203544_s_at | -0.922231323262765 | 0  |                | STAM        |
| 204082_at   | 0.910815804799754  | 0  |                | PBX3        |
| 219360_s_at | 0.902459945140701  | 0  |                | TRPM4       |
| 235604_x_at | -0.895150647295372 | 0  |                |             |
| 200742_s_at | 0.89214325035062   | 0  |                | CLN2        |
| 217520_x_at | 0.891291087387708  | 0  |                |             |

| AML MLL vs. CLL      |                   | samples: 15 / 32 |                |             |  |
|----------------------|-------------------|------------------|----------------|-------------|--|
| accuracy             | 1                 |                  |                |             |  |
| confidence           | 1                 |                  |                |             |  |
| gene                 | signal-to-noise   | p                | decision limit | gene symbol |  |
| 224838_at            | -3.80748815117863 | 0*               | 1810.6         |             |  |
| 212400_at            | -2.86025920523167 | 0                |                |             |  |
| 212827_at            | -2.83572202473321 | 0                |                | IGHM        |  |
| 223514_at            | -2.79698500849851 | 0                |                | CARD11      |  |
| 207168_s_at          | 2.78000663400662  | 0                |                | H2AFY       |  |
| 208456_s_at          | -2.77288752188536 | 0                |                | RRAS2       |  |
| 206111_at            | 2.74648404080317  | 0                |                | RNASE2      |  |
| 204951_at            | -2.73367910105826 | 0                |                | ARHH        |  |
| 204215_at            | -2.70725768797715 | 0                |                | MGC4175     |  |
| 41220_at             | -2.64744893915855 | 0                |                | MSF         |  |
| 227173_s_at          | -2.60156567650878 | 0                |                | BACH2       |  |
| 211404_s_at          | 2.58701495228114  | 0                |                | APLP2       |  |
| 201163_s_at          | 2.58627447208644  | 0                |                | IGFBP7      |  |
| 227829_at            | -2.5720529437702  | 0                |                |             |  |
| 202880_s_at          | -2.55714780536776 | 0                |                | PSCD1       |  |
| 224837_at            | -2.52465899436623 | 0                |                | FOXP1       |  |
| 209374_s_at          | -2.50451803785685 | 0                |                | IGHM        |  |
| 243780_at            | -2.49073709912546 | 0                |                |             |  |
| 212590_at            | -2.45765382458849 | 0                |                |             |  |
| AFFX-                |                   |                  |                |             |  |
| HUMGAPDH/M33197_3_at | -                 |                  |                |             |  |
| HG-U133B             | 2.15372303795555  | 0                |                | GAPD        |  |

## AML MLL vs. CML

samples: 15 / 14

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 209771_x_at | -4.47855739740896 | 0* | 4909           | CD24        |
| 216379_x_at | -4.47782401977517 | 0  |                |             |
| 212531_at   | -4.20914790815671 | 0  |                | LCN2        |
| 206676_at   | -4.08016979869995 | 0  |                | CEACAM8     |
| 205557_at   | -3.89666780981116 | 0  |                | BPI         |
| 209772_s_at | -3.7540800038095  | 0  |                | CD24        |
| 211657_at   | -3.35563391812807 | 0  |                |             |
| 203757_s_at | -3.27728001846237 | 0  |                | CEACAM6     |
| 202018_s_at | -3.2413562747036  | 0  |                | LTF         |
| 205513_at   | -3.11724133997788 | 0  |                | TCN1        |
| 207269_at   | -3.04676950166614 | 0  |                | DEFA4       |
| 207802_at   | -2.84753376114576 | 0  |                | SGP28       |
| 236908_at   | -2.83593202717857 | 0  |                |             |
| 266_s_at    | -2.75915771343774 | 0  |                | CD24        |
| 201105_at   | 2.73676787442809  | 0  |                | LGALS1      |
| 208890_s_at | 2.63909820141829  | 0  |                | PLXNB2      |
| 210244_at   | -2.58291056673136 | 0  |                | CAMP        |
| 214875_x_at | 2.54486223713713  | 0  |                | APLP2       |
| 236979_at   | -2.51234802423843 | 0  |                |             |
| 49306_at    | 1.35686961755716  | 0  |                | AD037       |

| AML MLL vs. normal BM |                   | samples: 15 / 9 |                |               |  |
|-----------------------|-------------------|-----------------|----------------|---------------|--|
| accuracy              | 1                 |                 |                |               |  |
| confidence            | 1                 |                 |                |               |  |
| gene                  | signal-to-noise   | p               | decision limit | gene symbol   |  |
| 225792_at             | -5.04037264761662 | 0*              | 76.45          |               |  |
| 227812_at             | -4.50172833847856 | 0               |                |               |  |
| 236908_at             | -4.3851399912751  | 0               |                |               |  |
| 225700_at             | -4.20778530270981 | 0               |                |               |  |
| 202018_s_at           | -4.1218976881036  | 0               |                | LTF           |  |
| 225804_at             | 3.78433665952281  | 0               |                |               |  |
| 212531_at             | -3.62189836886899 | 0               |                | LCN2          |  |
| 208651_x_at           | -3.08131561292721 | 0               |                | CD24          |  |
| 209771_x_at           | -2.80531442593767 | 0               |                | CD24          |  |
| 216379_x_at           | -2.74718662648409 | 0               |                |               |  |
| 210244_at             | -2.74600903663689 | 0               |                | CAMP          |  |
| 226301_at             | -2.70321745971481 | 0               |                | dJ55C23.6     |  |
| 227151_at             | 2.68181697471281  | 0               |                |               |  |
| 209160_at             | -2.64474285212333 | 0               |                | AKR1C3        |  |
| 225285_at             | -2.56569832423798 | 0               |                |               |  |
| 235818_at             | -2.5546546541523  | 0               |                |               |  |
| 226726_at             | -2.52741579223109 | 0               |                | LOC129642     |  |
| 207269_at             | -2.43598973973471 | 0               |                | DEFA4         |  |
| 226751_at             | -2.41273912703748 | 0               |                | DKFZP566K1924 |  |
| 58780_s_at            | 1.24593648437062  | 0               |                | FLJ10357      |  |

| AML MLL vs. ALL t(8;14) |                   | samples: 15 / 4 |                |             |  |
|-------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                | 1                 |                 |                |             |  |
| confidence              | 1                 |                 |                |             |  |
| gene                    | signal-to-noise   | p               | decision limit | gene symbol |  |
| 227173_s_at             | -2.97620214103741 | 0*              | 93.35          | BACH2       |  |
| 225700_at               | -2.97113581211542 | 0               |                |             |  |
| 212400_at               | -2.91449782508721 | 0               |                |             |  |
| 227151_at               | 2.68181697471281  | 0               |                |             |  |
| 205690_s_at             | -2.63484847538673 | 0               |                | G10         |  |
| 231552_at               | 2.60340424456959  | 0               |                |             |  |
| 239647_at               | 2.56381751217569  | 0               |                |             |  |
| 239835_at               | -2.49692099181388 | 0               |                | KIAA1842    |  |
| 226435_at               | 2.38716130768923  | 0               |                |             |  |
| 226301_at               | -2.38404537685874 | 0               |                | dJ55C23.6   |  |
| 226607_at               | 2.34518225140996  | 0               |                | L3MBTL      |  |
| 215785_s_at             | -2.31901965008779 | 0               |                | CYFIP2      |  |
| 225085_at               | 2.24977026547419  | 0               |                |             |  |
| 214651_s_at             | 2.24855870756181  | 0               |                | HOXA9       |  |
| 209765_at               | -2.20363939375933 | 0               |                | ADAM19      |  |
| 236606_at               | -2.19711183569464 | 0               |                |             |  |
| 218319_at               | -2.1925818315627  | 0               |                | PELI1       |  |
| 227525_at               | -2.16383106825606 | 0               |                | LOC113263   |  |
| 212538_at               | -2.11358391570231 | 0               |                | KIAA1058    |  |
| 228083_at               | 2.10218682980016  | 0               |                |             |  |

|                                 |                        |                 |                       |                    |
|---------------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>AML MLL vs. ALL B not Ph</b> |                        | samples: 15 / 9 |                       |                    |
| accuracy                        | 1                      |                 |                       |                    |
| confidence                      | 1                      |                 |                       |                    |
| <b>gene</b>                     | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 201482_at                       | 2.87636338319455       | 0*              | 363.95                | QSCN6              |
| 201105_at                       | 2.64910601922115       | 0               |                       | LGALS1             |
| 239647_at                       | 2.56381751217569       | 0               |                       |                    |
| 211404_s_at                     | 2.31189269578112       | 0               |                       | APLP2              |
| 201360_at                       | 2.27456235196276       | 0               |                       | CST3               |
| 214875_x_at                     | 2.20140608739693       | 0               |                       | APLP2              |
| 266_s_at                        | -2.19196810995278      | 0               |                       | CD24               |
| 208702_x_at                     | 2.17966631844281       | 0               |                       | APLP2              |
| 223469_at                       | 2.13015217253256       | 0               |                       | MGC10812           |
| 209771_x_at                     | -2.12750959401045      | 0               |                       | CD24               |
| 208248_x_at                     | 2.10716186347527       | 0               |                       | APLP2              |
| 230441_at                       | -2.03717805375485      | 0               |                       |                    |
| 200742_s_at                     | 2.01183913393136       | 0               |                       | CLN2               |
| 216379_x_at                     | -1.97574478072792      | 0               |                       |                    |
| 204215_at                       | -1.96532146024999      | 0               |                       | MGC4175            |
| 208650_s_at                     | -1.93906624919753      | 0               |                       | CD24               |
| 214651_s_at                     | 1.92853927147488       | 0               |                       | HOXA9              |
| 233813_at                       | -1.8799760260639       | 0               |                       |                    |
| 208703_s_at                     | 1.86864966354898       | 0               |                       | APLP2              |
| 58780_s_at                      | 1.40471564488899       | 0               |                       | FLJ10357           |



| AML MLL vs. ALL Ph |                   | samples: 15 / 15 |                |             |  |
|--------------------|-------------------|------------------|----------------|-------------|--|
| accuracy           | 1                 |                  |                |             |  |
| confidence         | 1                 |                  |                |             |  |
| gene               | signal-to-noise   | p                | decision limit | gene symbol |  |
| 210487_at          | -2.66400596339357 | 0                |                | DNTT        |  |
| 211404_s_at        | 2.5799328562955   | 0                |                | APLP2       |  |
| 214875_x_at        | 2.53091704146699  | 0                |                | APLP2       |  |
| 208702_x_at        | 2.442063176235    | 0                |                | APLP2       |  |
| 214651_s_at        | 2.38931027314895  | 0                |                | HOXA9       |  |
| 234107_s_at        | 2.17019003130007  | 0*               | 321.6          | LGALS1      |  |
| 201105_at          | 2.08770407459668  | 0                |                |             |  |
| 239647_at          | 2.02467198705529  | 0                |                |             |  |
| 217979_at          | -1.99927745769533 | 0                |                | NET-6       |  |
| 213150_at          | 1.98436589229381  | 0                |                | HOXA10      |  |
| 212012_at          | -1.96026252932157 | 0                |                | D2S448      |  |
| 207971_s_at        | -1.95442302553682 | 0                |                | KIAA0582    |  |
| 200742_s_at        | 1.93172870108821  | 0                |                | CLN2        |  |
| 236606_at          | -1.90758120714248 | 0                |                |             |  |
| 235753_at          | 1.89768662161529  | 0                |                |             |  |
| 232035_at          | -1.87493486925109 | 0                |                | H4FH        |  |
| 41220_at           | -1.84432301556426 | 0                |                | MSF         |  |
| 209771_x_at        | -1.83370834497243 | 0                |                | CD24        |  |
| 1007_s_at          | -1.8257200735147  | 0                |                | DDR1        |  |
| 201968_s_at        | 1.81818231032019  | 0                |                | PGM1        |  |

## AML MLL vs. T-ALL

samples: 15 / 9

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 242292_at   | -3.53231266693437 | 0* | 19.4           |             |
| 243154_at   | -3.1306973304726  | 0  |                |             |
| 219891_at   | 3.05552709838153  | 0  |                | FLJ20208    |
| 211404_s_at | 2.9355923181049   | 0  |                | APLP2       |
| 209499_x_at | 2.75677919960856  | 0  |                | TNFSF13     |
| 211495_x_at | 2.73018317509301  | 0  |                | TNFSF13     |
| 208702_x_at | 2.59886997802643  | 0  |                | APLP2       |
| 214875_x_at | 2.52933264502392  | 0  |                | APLP2       |
| 206111_at   | 2.43695278026584  | 0  |                | RNASE2      |
| 209500_x_at | 2.41035664982945  | 0  |                | TNFSF13     |
| 210314_x_at | 2.38921906328214  | 0  |                | TNFSF13     |
| 225003_at   | 2.37212829914098  | 0  |                | MBC3205     |
| 218122_s_at | -2.30056189156697 | 0  |                | SENP2       |
| 204484_at   | -2.28386643829897 | 0  |                | PIK3C2B     |
| 205640_at   | 2.26383232065516  | 0  |                | ALDH3B1     |
| 201105_at   | 2.26087708407154  | 0  |                | LGALS1      |
| 200743_s_at | 2.25956196871586  | 0  |                | CLN2        |
| 222698_s_at | 2.23788003936299  | 0  |                | IMPACT      |
| 200742_s_at | 2.2220970534291   | 0  |                | CLN2        |
| 201537_s_at | 2.16766347414866  | 0  |                | DUSP3       |

|                                 |                   |                  |                |             |
|---------------------------------|-------------------|------------------|----------------|-------------|
| AML MLL vs. AML +8              |                   | samples: 15 / 10 |                |             |
| accuracy                        | 1                 |                  |                |             |
| confidence                      | 0.8689072208975   |                  |                |             |
| gene                            | signal-to-noise   | p                | decision limit | gene symbol |
| 200056_s_at - HG-U133A          | -1.60303643777462 | 0                |                | C1D         |
| 212250_at                       | -1.47262825515036 | 0                |                |             |
| 228024_at                       | -1.43968630786794 | 0                |                | PAK1        |
| 205355_at                       | -1.39534301157978 | 0                |                | ACADSB      |
| 225700_at                       | -1.39419450937928 | 0.01             |                |             |
| 234726_s_at                     | 1.36257922965513  | 0                |                |             |
| 202619_s_at                     | -1.34323877280623 | 0                |                | PLOD2       |
| 205453_at                       | -1.29520111839967 | 0                |                | HOXB2       |
| 202823_at                       | -1.28255326311509 | 0                |                | TCEB1       |
| 210749_x_at                     | -1.26893758929818 | 0                |                | DDR1        |
| 227786_at                       | -1.24020773870069 | 0                |                | TRAP25      |
| 212479_s_at                     | -1.23922427261637 | 0*               | 437.3          | FLJ13910    |
| 219312_s_at                     | -1.21983738431424 | 0                |                | RINZF       |
| 218172_s_at                     | -1.21403337241271 | 0*               | 285.95         | PRO2577     |
| 200867_at                       | -1.2110165320696  | 0*               | 531            |             |
| 202956_at                       | -1.21043821718202 | 0*               | 550.6          | BIG1        |
| 213902_at                       | -1.19710457307816 | 0                |                | ASAH        |
| 239597_at                       | 1.19444081572455  | 0                |                |             |
| 214789_x_at                     | -1.19367799101574 | 0                |                | SRP46       |
| AFFX-r2-Ec-bioD-3_at - HG-U133B | 0.789398697044362 | 0                |                |             |

| AML MLL vs. AML complex |                   | samples: 15 / 36 |                |             |  |
|-------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                | 1                 |                  |                |             |  |
| confidence              | 0.928537448772464 |                  |                |             |  |
| gene                    | signal-to-noise   | p                | decision limit | gene symbol |  |
| 228083_at               | 1.83691594955677  | 0                |                |             |  |
| 201105_at               | 1.56013660814198  | 0                |                | LGALS1      |  |
| 201377_at               | -1.5390279619994  | 0                |                | KIAA0144    |  |
| 201358_s_at             | -1.46121373620596 | 0                |                | COPB        |  |
| 203387_s_at             | -1.43200690176451 | 0                |                | KIAA0603    |  |
| 201585_s_at             | -1.42612880048733 | 0                |                | SFPQ        |  |
| 222982_x_at             | -1.4232823410753  | 0                |                | SLC38A2     |  |
| 202746_at               | -1.40541613814493 | 0*               | 277.15         |             |  |
| 204951_at               | -1.38290450200254 | 0*               | 224.05         | ARHH        |  |
| 203725_at               | -1.35090921185734 | 0                |                | GADD45A     |  |
| 203544_s_at             | -1.33195316834084 | 0                |                | STAM        |  |
| 225804_at               | 1.3109814684568   | 0                |                |             |  |
| 203386_at               | -1.30903268579411 | 0                |                | KIAA0603    |  |
| 201359_at               | -1.3066438308133  | 0                |                | COPB        |  |
| 201830_s_at             | -1.29170882160348 | 0                |                | NET1        |  |
| 218041_x_at             | -1.27263528593652 | 0                |                | PRO1068     |  |
| 223318_s_at             | 1.27042416454958  | 0                |                | MGC10974    |  |
| 212222_at               | -1.26786775770503 | 0                |                | KIAA0077    |  |
| 201829_at               | -1.26235979300155 | 0                |                | NET1        |  |
| 239647_at               | 1.09622576767215  | 0                |                |             |  |

|                               |                        |                   |                       |                    |  |
|-------------------------------|------------------------|-------------------|-----------------------|--------------------|--|
| <b>AML MLL vs. AML normal</b> |                        | samples: 15 / 62  |                       |                    |  |
| accuracy                      |                        | 0.948051948051948 |                       |                    |  |
| confidence                    |                        | 0.903617550418171 |                       |                    |  |
| failed:                       |                        | 3,4,72,76         |                       |                    |  |
| <b>gene</b>                   | <b>signal-to-noise</b> | <b>p</b>          | <b>decision limit</b> | <b>gene symbol</b> |  |
| 205453_at                     | -1.38558116676561      | 0*                | 203.25                | HOXB2              |  |
| 222465_at                     | -1.29236441992376      | 0                 |                       | C15orf15           |  |
| 225406_at                     | -1.29036630213613      | 0*                | 191.3                 | TSG                |  |
| 200829_x_at                   | -1.1349148684836       | 0                 |                       | ZNF207             |  |
| 225326_at                     | -1.12776286034489      | 0                 |                       | KIAA1311           |  |
| 200056_s_at - HG-U133B        | -1.12696320763032      | 0                 |                       | C1D                |  |
| 238856_s_at                   | -1.09612740485765      | 0                 |                       |                    |  |
| 227786_at                     | -1.08912698999125      | 0                 |                       | TRAP25             |  |
| 200673_at                     | -1.08754065564232      | 0                 |                       | LAPTM4A            |  |
| 226250_at                     | -1.08598948671591      | 0                 |                       |                    |  |
| 233559_s_at                   | 1.08564709559314       | 0                 |                       | FENS-1             |  |
| 228904_at                     | -1.07283266172579      | 0                 |                       |                    |  |
| 227680_at                     | -1.06344466244967      | 0                 |                       |                    |  |
| 223982_s_at                   | -1.06119523760418      | 0                 |                       | IPLA2              |  |
| 202377_at                     | -1.05377199670316      | 0                 |                       | HSOBRGRP           |  |
| 225700_at                     | -1.04818024157045      | 0                 |                       |                    |  |
| 209160_at                     | -1.04660040264575      | 0                 |                       | AKR1C3             |  |
| 229232_at                     | -1.04476453216419      | 0                 |                       |                    |  |
| 231870_s_at                   | -1.04348230442961      | 0                 |                       | LOC51068           |  |
| 201105_at                     | 1.03632090944134       | 0                 |                       | LGALS1             |  |

| AML MLL vs. AML t(8;21) |                   | samples: 15 / 13 |                |             |  |
|-------------------------|-------------------|------------------|----------------|-------------|--|
| accuracy                | 1                 |                  |                |             |  |
| confidence              | 1                 |                  |                |             |  |
| gene                    | signal-to-noise   | p                | decision limit | gene symbol |  |
| 214651_s_at             | 2.42114497347366  | 0                |                | HOXA9       |  |
| 201105_at               | 2.17374439391796  | 0*               | 3881.25        | LGALS1      |  |
| 228827_at               | -2.03460798747208 | 0                |                |             |  |
| 206009_at               | -2.02655766969028 | 0                |                | ITGA9       |  |
| 228083_at               | 1.99768244710951  | 0                |                |             |  |
| 213150_at               | 1.98436589229381  | 0                |                | HOXA10      |  |
| 50221_at                | 1.94810783752319  | 0                |                |             |  |
| 221581_s_at             | 1.89677192380517  | 0                |                | WBSCR5      |  |
| 235753_at               | 1.88396584115232  | 0                |                |             |  |
| 206622_at               | -1.79659162526109 | 0                |                | TRH         |  |
| 209905_at               | 1.76718971964498  | 0                |                | HOXA9       |  |
| 204069_at               | 1.75588643276789  | 0                |                | MEIS1       |  |
| 209160_at               | -1.75500319419551 | 0                |                | AKR1C3      |  |
| 235818_at               | -1.70111545046162 | 0                |                |             |  |
| 223498_at               | 1.67798456165549  | 0                |                |             |  |
| 211404_s_at             | 1.67488607654784  | 0                |                | APLP2       |  |
| 209500_x_at             | 1.66210516483391  | 0                |                | TNFSF13     |  |
| 203949_at               | -1.65967693892027 | 0                |                | MPO         |  |
| 214875_x_at             | 1.65852470588382  | 0                |                | APLP2       |  |
| 56256_at                | 1.09757984221605  | 0                |                | LOC51092    |  |

|                   |                   |    |                |               |  |
|-------------------|-------------------|----|----------------|---------------|--|
| CLL vs. all other | samples: 32 / 237 |    |                |               |  |
| accuracy          | 0.996282527881041 |    |                |               |  |
| confidence        | 1                 |    |                |               |  |
| failed:           | 11                |    |                |               |  |
| gene              | signal-to-noise   | p  | decision limit | gene symbol   |  |
| 224838_at         | 2.72658457901213  | 0  | 630.55         |               |  |
| 239287_at         | 2.21787255431445  | 0* |                |               |  |
| 223514_at         | 2.1294564890461   | 0  |                | CARD11        |  |
| 44790_s_at        | 2.04322734300157  | 0  |                | FLJ21562      |  |
| 212590_at         | 2.0395652222237   | 0  |                |               |  |
| 223287_s_at       | 2.01927297186102  | 0  |                | FOXP1         |  |
| 228390_at         | 2.01736536531344  | 0  |                |               |  |
| 219471_at         | 2.0123024445387   | 0  |                | FLJ21562      |  |
| 208456_s_at       | 2.00649246957273  | 0  |                | RRAS2         |  |
| 243780_at         | 1.99741020732395  | 0  |                |               |  |
| 201998_at         | 1.97818562004593  | 0  |                | SIAT1         |  |
| 223391_at         | 1.97429784627482  | 0  |                | LOC81537      |  |
| 208091_s_at       | 1.95442592300049  | 0  |                | DKFZP564K0822 |  |
| 225927_at         | 1.94521013683932  | 0  |                | MAP3K1        |  |
| 202589_at         | -1.94332001129586 | 0  |                | TYMS          |  |
| 229072_at         | 1.94278755168998  | 0  |                |               |  |
| 229844_at         | 1.93701311168151  | 0  |                |               |  |
| 214615_at         | 1.91900370555866  | 0  |                | P2Y10         |  |
| 230768_at         | 1.89700621262016  | 0  |                |               |  |
| 224837_at         | 1.88521474574714  | 0  |                | FOXP1         |  |

|                    |                        |                  |                       |                    |
|--------------------|------------------------|------------------|-----------------------|--------------------|
| <b>CLL vs. CML</b> |                        | samples: 32 / 14 |                       |                    |
| accuracy           | 1                      |                  |                       |                    |
| confidence         | 1                      |                  |                       |                    |
| <b>gene</b>        | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 210254_at          | -4.88339464327865      | 0*               | 3718.45               |                    |
| 205557_at          | -4.67296996074416      | 0                |                       | BPI                |
| 206111_at          | -4.55904506479679      | 0                |                       | RNASE2             |
| 209619_at          | 4.54717160557061       | 0                |                       | CD74               |
| 202503_s_at        | -4.46030015155587      | 0                |                       | KIAA0101           |
| 206871_at          | -4.43465869214911      | 0                |                       | ELA2               |
| 203949_at          | -4.36878588501229      | 0                |                       | MPO                |
| 202589_at          | -4.25959896335016      | 0                |                       | TYMS               |
| 212268_at          | -4.11824280019806      | 0                |                       | SERPINB1           |
| 212531_at          | -4.10884128760506      | 0                |                       | LCN2               |
| 206676_at          | -3.98482491918087      | 0                |                       | CEACAM8            |
| 204670_x_at        | 3.97453356450998       | 0                |                       | HLA-DRB5           |
| 210334_x_at        | -3.95114669210453      | 0                |                       | BIRC5              |
| 200654_at          | -3.73551197850169      | 0                |                       | P4HB               |
| 208306_x_at        | 3.6021607716515        | 0                |                       | HLA-DRB4           |
| 224838_at          | 3.57587529198941       | 0                |                       |                    |
| 213572_s_at        | -3.56773642902922      | 0                |                       | SERPINB1           |
| 207269_at          | -3.5389139132598       | 0                |                       | DEFA4              |
| 212750_at          | 3.51249429987917       | 0                |                       | PPP1R16B           |
| 41577_at           | 3.13666804152596       | 0                |                       | PPP1R16B           |



## CLL vs. normal BM

samples: 32 / 9

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 204776_at   | -4.80025506569938 | 0* | 163.3          | THBS4       |
| 210613_s_at | -4.76199342875923 | 0  |                | SYNGR1      |
| 218662_s_at | -4.49242317171143 | 0  |                | HCAP-G      |
| 202503_s_at | -4.2272639947421  | 0  |                | KIAA0101    |
| 202580_x_at | -4.18939678293477 | 0  |                | FOXN1       |
| 205051_s_at | -4.15661524563327 | 0  |                | KIT         |
| 202018_s_at | -4.09501572722927 | 0  |                | LTF         |
| 230988_at   | -4.0486666186669  | 0  |                |             |
| 206871_at   | -4.04477996703664 | 0  |                | ELA2        |
| 224975_at   | -3.78270966714705 | 0  |                | NFIA        |
| 227230_s_at | -3.69195069014622 | 0  |                | KIAA1211    |
| 209714_s_at | -3.55884052493629 | 0  |                | CDKN3       |
| 212531_at   | -3.54256621978711 | 0  |                | LCN2        |
| 214575_s_at | -3.53838586077798 | 0  |                | AZU1        |
| 202589_at   | -3.38277320357567 | 0  |                | TYMS        |
| 223785_at   | -3.37348567040386 | 0  |                | FLJ10719    |
| 202705_at   | -3.36111245088024 | 0  |                | CCNB2       |
| 224976_at   | -3.35971882977735 | 0  |                | NFIA        |
| 210052_s_at | -3.33990497740824 | 0  |                | C20orf1     |

## CLL vs. ALL t(8;14)

samples: 32 / 4

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 202580_x_at | -7.18159480292423 | 0* | 218.2          | FOXN1       |
| 209891_at   | -6.98895220029526 | 0  |                | AD024       |
| 227039_at   | 3.70691051731571  | 0  |                | AKAP13      |
| 218663_at   | -3.68808195572391 | 0  |                | HCAP-G      |
| 36004_at    | 3.51464925040429  | 0  |                | IKBKG       |
| 226936_at   | -3.44796352148406 | 0  |                |             |
| 228211_at   | 3.34271829518438  | 0  |                |             |
| 218355_at   | -3.32490989672808 | 0  |                | KIF4A       |
| 201761_at   | -3.28097759120759 | 0  |                | MTHFD2      |
| 205837_s_at | -3.18161701452463 | 0  |                | GYPA        |
| 210052_s_at | -3.16637659493241 | 0  |                | C20orf1     |
| 202095_s_at | -3.11748537316183 | 0  |                | BIRC5       |
| 202503_s_at | -3.09625623775405 | 0  |                | KIAA0101    |
| 212020_s_at | -3.09152886109552 | 0  |                | MKI67       |
| 216833_x_at | -3.08262837314566 | 0  |                |             |
| 228361_at   | -3.05435230901633 | 0  |                |             |
| 212022_s_at | -3.01225907956052 | 0  |                | MKI67       |
| 227065_at   | 3.00267996592052  | 0  |                | COL5A2      |
| 218039_at   | -2.9948995053224  | 0  |                | ANKT        |
| 36920_at    | 2.10655917810938  | 0  |                | MTM1        |

|                             |                        |                 |                       |                    |
|-----------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>CLL vs. ALL B not Ph</b> |                        | samples: 32 / 9 |                       |                    |
| accuracy                    | 1                      |                 |                       |                    |
| confidence                  | 1                      |                 |                       |                    |
| <b>gene</b>                 | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 225927_at                   | 3.15130564055876       | 0*              | 1541.45               | MAP3K1             |
| 213927_at                   | 2.64985304902657       | 0               |                       |                    |
| 201462_at                   | 2.62143810029708       | 0               |                       | KIAA0193           |
| 224838_at                   | 2.5941283416844        | 0               |                       |                    |
| 213453_x_at                 | -2.18846578413759      | 0               |                       | GAPD               |
| 239287_at                   | 2.18590081196116       | 0               |                       |                    |
| 208091_s_at                 | 2.12019333022318       | 0               |                       | DKFZP564K0822      |
| 201998_at                   | 2.1165316341122        | 0               |                       | SIAT1              |
| 224848_at                   | -2.11049474415864      | 0               |                       |                    |
| 202863_at                   | 2.08665988043685       | 0               |                       | SP100              |
| 225592_at                   | -2.07634399767076      | 0               |                       | NRM                |
| 205805_s_at                 | 2.04616469387812       | 0               |                       | ROR1               |
| 228390_at                   | 2.03697588799482       | 0               |                       |                    |
| AFFX-                       |                        |                 |                       |                    |
| HUMGAPDH/M33197_3_at        | -                      |                 |                       |                    |
| HG-U133B                    | -2.02578116307399      | 0               |                       | GAPD               |
| 220768_s_at                 | 2.01657972292803       | 0               |                       | CSNK1G3            |
| 221858_at                   | 2.00702836396881       | 0               |                       | KIAA0608           |
| 214786_at                   | 2.00594347120247       | 0               |                       | MAP3K1             |
| 224570_s_at                 | -2.00161337456916      | 0               |                       |                    |
| 202625_at                   | 1.99700437780915       | 0               |                       | LYN                |
| AFFX-r2-Hs18SrRNA-3_s_at -  |                        |                 |                       |                    |
| HG-U133B                    | 0.670536484443349      | 0               |                       |                    |

|                       |                        |                  |                       |                    |
|-----------------------|------------------------|------------------|-----------------------|--------------------|
| <b>CLL vs. ALL Ph</b> |                        | samples: 32 / 15 |                       |                    |
| accuracy              | 1                      |                  |                       |                    |
| confidence            | 1                      |                  |                       |                    |
| <b>gene</b>           | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 204663_at             | -3.923285216392        | 0*               | 80.55                 | ME3                |
| 203373_at             | -3.78247945374324      | 0                |                       | STAT12             |
| 225927_at             | 3.05858766321181       | 0                |                       | MAP3K1             |
| 223514_at             | 2.79698500849851       | 0                |                       | CARD11             |
| 210487_at             | -2.66400596339357      | 0                |                       | DNTT               |
| 213927_at             | 2.64985304902657       | 0                |                       |                    |
| 237337_at             | 2.52705433891484       | 0                |                       |                    |
| 236280_at             | 2.49746424904494       | 0                |                       |                    |
| 227900_at             | 2.49040043479395       | 0                |                       |                    |
| 211709_s_at           | -2.45092080989795      | 0                |                       | SCGF               |
| 224833_at             | 2.40705165058966       | 0                |                       | ETS1               |
| 226545_at             | -2.40457551567713      | 0                |                       |                    |
| 208091_s_at           | 2.38274758846201       | 0                |                       | DKFZP564K0822      |
| 235674_at             | 2.37963455734461       | 0                |                       |                    |
| 234107_s_at           | 2.36302665773918       | 0                |                       |                    |
| 223462_at             | 2.32337125093609       | 0                |                       | MGC4618            |
| 201462_at             | 2.3212369641096        | 0                |                       | KIAA0193           |
| 223391_at             | 2.30224083750022       | 0                |                       | LOC81537           |
| 212719_at             | -2.29194173393375      | 0                |                       | SCOP               |

|                      |                        |                 |                       |                    |
|----------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>CLL vs. T-ALL</b> |                        | samples: 32 / 9 |                       |                    |
| accuracy             | 1                      |                 |                       |                    |
| confidence           | 1                      |                 |                       |                    |
| <b>gene</b>          | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 201417_at            | -3.83747798152129      | 0*              | 2230.95               |                    |
| 201416_at            | -3.69716215884899      | 0               |                       | SOX4               |
| 221858_at            | 2.73818494452306       | 0               |                       | KIAA0608           |
| 213772_s_at          | 2.72201152228286       | 0               |                       | GGA2               |
| 224932_at            | 2.6366912338985        | 0               |                       | PRSS2              |
| 224847_at            | -2.63602874545103      | 0               |                       |                    |
| 201462_at            | 2.62143810029708       | 0               |                       | KIAA0193           |
| 224848_at            | -2.60776696130397      | 0               |                       |                    |
| 243780_at            | 2.49991585531364       | 0               |                       |                    |
| 227900_at            | 2.49040043479395       | 0               |                       |                    |
| 202625_at            | 2.4377901797746        | 0               |                       | LYN                |
| 228390_at            | 2.41659743191322       | 0               |                       |                    |
| 201998_at            | 2.39630335572289       | 0               |                       | SIAT1              |
| 226545_at            | -2.3815195487075       | 0               |                       |                    |
| 204446_s_at          | 2.37716091038765       | 0               |                       | ALOX5              |
| 204192_at            | 2.34749349754959       | 0               |                       | CD37               |
| 219076_s_at          | -2.31227318629435      | 0               |                       | PXMP2              |
| 206398_s_at          | 2.30227312148638       | 0               |                       | CD19               |
| 224838_at            | 2.29208011575118       | 0               |                       |                    |
| 212827_at            | 2.28758794629918       | 0               |                       | IGHM               |

## CLL vs. AML +8

samples: 32 / 10

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol   |
|-------------|-------------------|----|----------------|---------------|
| 224838_at   | 3.16933404672116  | 0  |                |               |
| 223514_at   | 2.79698500849851  | 0  |                | CARD11        |
| 212827_at   | 2.5676577800083   | 0  |                | IGHM          |
| 201200_at   | -2.5208800664045  | 0  |                | CREG          |
| 242633_x_at | 2.38085767453167  | 0  |                |               |
| 208456_s_at | 2.34106774724323  | 0  |                | RRAS2         |
| 212590_at   | 2.3295599530646   | 0  |                |               |
| 44790_s_at  | 2.32854069014676  | 0  |                | FLJ21562      |
| 219471_at   | 2.27189811261511  | 0  |                | FLJ21562      |
| 202441_at   | -2.26915475899159 | 0  |                | KEO4          |
| 209374_s_at | 2.26352755463127  | 0  |                | IGHM          |
| 243780_at   | 2.25989352775893  | 0  |                |               |
| 204215_at   | 2.24311505389492  | 0* | 906.65         | MGC4175       |
| 223382_s_at | -2.21844659554677 | 0  |                | NIN283        |
| 201163_s_at | -2.2061831531108  | 0  |                | IGFBP7        |
| 224837_at   | 2.17714293481922  | 0  |                | FOXP1         |
| 223391_at   | 2.1733535915887   | 0  |                | LOC81537      |
| 208091_s_at | 2.17150813050761  | 0  |                | DKFZP564K0822 |
| 205933_at   | 2.16573909337041  | 0  |                | SETBP1        |
| 239287_at   | 2.1598880074389   | 0  |                |               |

|                            |                        |                  |                       |                    |
|----------------------------|------------------------|------------------|-----------------------|--------------------|
| <b>CLL vs. AML complex</b> |                        | samples: 32 / 36 |                       |                    |
| accuracy                   | 1                      |                  |                       |                    |
| confidence                 | 1                      |                  |                       |                    |
| <b>gene</b>                | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 224838_at                  | 2.78969388721613       | 0                |                       |                    |
| 235674_at                  | 2.37963455734461       | 0                |                       |                    |
| 243780_at                  | 2.32051881321218       | 0                |                       |                    |
| 239287_at                  | 2.24074490580899       | 0                |                       |                    |
| 223514_at                  | 2.18755403591948       | 0                |                       | CARD11             |
| 222680_s_at                | -2.18354473266858      | 0*               | 203.95                | RAMP               |
| 209619_at                  | 2.13206191976271       | 0                |                       | CD74               |
| 202503_s_at                | -2.11188972263141      | 0                |                       | KIAA0101           |
| 208456_s_at                | 2.10620770802115       | 0                |                       | RRAS2              |
| 208864_s_at                | -2.10162761752294      | 0                |                       | TXN                |
| 212590_at                  | 2.09310293747601       | 0                |                       |                    |
| 201200_at                  | -2.05492899324696      | 0                |                       | CREG               |
| 212827_at                  | 2.05442625446282       | 0                |                       | IGHM               |
| 224837_at                  | 2.04951179193956       | 0                |                       | FOXP1              |
| 205805_s_at                | 2.04616469387812       | 0                |                       | ROR1               |
| 244261_at                  | 2.03144018714413       | 0                |                       |                    |
| 223287_s_at                | 2.0252763158281        | 0                |                       | FOXP1              |
| 208091_s_at                | 2.0139098675012        | 0                |                       | DKFZP564K0822      |
| 226989_at                  | 2.00631003964875       | 0                |                       |                    |
| 236854_at                  | 1.99292097643003       | 0                |                       |                    |

| <b>CLL vs. AML normal</b> | samples: 32 / 62  |    |                |             |
|---------------------------|-------------------|----|----------------|-------------|
| accuracy                  | 0.98936170212766  |    |                |             |
| confidence                | 1                 |    |                |             |
| failed:                   | 11                |    |                |             |
| gene                      | signal-to-noise   | p  | decision limit | gene symbol |
| 224838_at                 | 2.80936017892095  | 0* | 2987.7         |             |
| 243780_at                 | 2.42900650257202  | 0  |                |             |
| 223514_at                 | 2.40431982389629  | 0  |                | CARD11      |
| 201200_at                 | -2.28363968538296 | 0  |                | CREG        |
| 201998_at                 | 2.19987941765164  | 0  |                | SIAT1       |
| 44790_s_at                | 2.18842053042545  | 0  |                | FLJ21562    |
| 205049_s_at               | 2.18662155440889  | 0  |                | CD79A       |
| 239287_at                 | 2.17948863877979  | 0  |                |             |
| 223287_s_at               | 2.16628667951355  | 0  |                | FOXP1       |
| 223391_at                 | 2.16298199717166  | 0  |                | LOC81537    |
| 219471_at                 | 2.13618332752253  | 0  |                | FLJ21562    |
| 225175_s_at               | 2.12811708839772  | 0  |                | CTL2        |
| 204215_at                 | 2.11642877909845  | 0  |                | MGC4175     |
| 236280_at                 | 2.11271003733104  | 0  |                |             |
| 208456_s_at               | 2.10890038745727  | 0  |                | RRAS2       |
| 206398_s_at               | 2.09984081904119  | 0  |                | CD19        |
| 212827_at                 | 2.09850222830603  | 0  |                | IGHM        |
| 228390_at                 | 2.09600254213173  | 0  |                |             |
| 229072_at                 | 2.09351406943008  | 0  |                |             |
| 214615_at                 | 2.06329249104139  | 0  |                | P2Y10       |



|                            |                        |                  |                       |                    |
|----------------------------|------------------------|------------------|-----------------------|--------------------|
| <b>CLL vs. AML t(8;21)</b> |                        | samples: 32 / 13 |                       |                    |
| accuracy                   | 1                      |                  |                       |                    |
| confidence                 | 1                      |                  |                       |                    |
| <b>gene</b>                | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 203949_at                  | -3.50330789770673      | 0                | 113.25                | MPO                |
| 224838_at                  | 3.25663434332492       | 0                |                       |                    |
| 205192_at                  | 3.21758439151756       | 0*               |                       | MAP3K14            |
| 211709_s_at                | -2.95109939287116      | 0                |                       | SCGF               |
| 212827_at                  | 2.84469338495376       | 0                |                       | IGHM               |
| 230768_at                  | 2.8154401362934        | 0                |                       |                    |
| 206009_at                  | -2.7972720292112       | 0                |                       | ITGA9              |
| 208091_s_at                | 2.63085873400942       | 0                |                       | DKFZP564K0822      |
| 208456_s_at                | 2.62810675193075       | 0                |                       | RRAS2              |
| 215215_s_at                | -2.60039836996497      | 0                |                       |                    |
| 203948_s_at                | -2.56960807932381      | 0                |                       | MPO                |
| 201811_x_at                | 2.56895859687937       | 0                |                       | SH3BP5             |
| 243780_at                  | 2.51082778037667       | 0                |                       |                    |
| 212590_at                  | 2.50058834205242       | 0                |                       |                    |
| 227900_at                  | 2.49040043479395       | 0                |                       |                    |
| 226546_at                  | -2.44432895386159      | 0                |                       |                    |
| 225927_at                  | 2.44085004959256       | 0                |                       | MAP3K1             |
| 212589_at                  | 2.43561411833392       | 0                |                       | RRAS2              |
| 228390_at                  | 2.41659743191322       | 0                |                       |                    |
| 225246_at                  | 2.39661265710521       | 0                |                       | STIM2              |

| <b>CML vs. all other</b> | samples: 14 / 255 |    |                |             |
|--------------------------|-------------------|----|----------------|-------------|
| accuracy                 | 0.981412639405205 |    |                |             |
| confidence               | 0.984251851969928 |    |                |             |
| failed:                  | 4,6,10,14,115     |    |                |             |
| gene                     | signal-to-noise   | p  | decision limit | gene symbol |
| 212531_at                | 2.20686225450673  | 0  |                | LCN2        |
| 205557_at                | 2.19817622063178  | 0* | 11581.65       | BPI         |
| 206676_at                | 2.01751329912518  | 0  |                | CEACAM8     |
| 209772_s_at              | 1.89825970350824  | 0* | 3429.4         | CD24        |
| 207802_at                | 1.84335905687648  | 0  |                | SGP28       |
| 216379_x_at              | 1.76253321043545  | 0  |                |             |
| 209771_x_at              | 1.75699226119665  | 0  |                | CD24        |
| 203936_s_at              | 1.75554347155831  | 0  |                | MMP9        |
| 211657_at                | 1.69149085236384  | 0  |                |             |
| 203757_s_at              | 1.6780512743379   | 0  |                | CEACAM6     |
| 210254_at                | 1.6590320804534   | 0  |                |             |
| 202018_s_at              | 1.64680728641866  | 0  |                | LTF         |
| 211275_s_at              | 1.62477051547664  | 0  |                | GYG         |
| 205513_at                | 1.60415014432038  | 0  |                | TCN1        |
| 205863_at                | 1.60339454990244  | 0  |                | S100A12     |
| 223839_s_at              | 1.57424844312026  | 0  |                |             |
| 210244_at                | 1.56058501019954  | 0  |                | CAMP        |
| 206440_at                | 1.5590538838617   | 0  |                | VELI1       |
| 207269_at                | 1.55083422089021  | 0  |                | DEFA4       |
| 204174_at                | 1.53747851176966  | 0  |                | ALOX5AP     |

|                          |                        |                 |                       |                    |
|--------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>CML vs. normal BM</b> |                        | samples: 14 / 9 |                       |                    |
| accuracy                 | 1                      |                 |                       |                    |
| confidence               | 1                      |                 |                       |                    |
| <b>gene</b>              | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 227198_at                | -3.96995770729437      | 0*              | 39.95                 |                    |
| 204562_at                | -3.83910818190111      | 0               |                       | IRF4               |
| 227749_at                | -3.11980636745679      | 0               |                       |                    |
| 228377_at                | -2.65145492785893      | 0               |                       | KIAA1384           |
| 226713_at                | -2.28229285614419      | 0               |                       |                    |
| 209619_at                | -2.27384420268273      | 0               |                       | CD74               |
| 227375_at                | -2.22184735546056      | 0               |                       | DKFZP566D1346      |
| 204057_at                | -2.13119125485664      | 0               |                       | ICSBP1             |
| 201506_at                | -2.05058862618543      | 0               |                       | TGFB1              |
| 221558_s_at              | -2.0055054625083       | 0               |                       | LEF1               |
| 227867_at                | -2.00414646646454      | 0               |                       |                    |
| 225331_at                | -1.95134035825926      | 0               |                       |                    |
| 223280_x_at              | -1.95125537387335      | 0               |                       | MS4A6A             |
| 243780_at                | -1.94601159348593      | 0               |                       |                    |
| 228055_at                | -1.94418493221925      | 0               |                       |                    |
| 204670_x_at              | -1.94197079510435      | 0               |                       | HLA-DRB5           |
| 208683_at                | -1.93662356244796      | 0               |                       | CAPN2              |
| 210356_x_at              | -1.92014292171279      | 0               |                       | MS4A2              |
| 209670_at                | -1.89146017871026      | 0               |                       | TRA                |
| AFFX-                    |                        |                 |                       |                    |
| HUMGAPDH/M33197_3_at     | -                      |                 |                       |                    |
| HG-U133B                 | 1.0887744230798        | 0               |                       | GAPD               |

| CML vs. ALL t(8;14) |                   | samples: 14 / 4 |                |             |  |
|---------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy            | 1                 |                 |                |             |  |
| confidence          | 1                 |                 |                |             |  |
| gene                | signal-to-noise   | p               | decision limit | gene symbol |  |
| 231215_at           | -3.69904177219169 | 0*              | 17.25          |             |  |
| 212400_at           | -3.60679086659289 | 0               |                |             |  |
| 239835_at           | -3.24273732421016 | 0               |                | KIAA1842    |  |
| 214439_x_at         | -3.01379256143662 | 0               |                | BIN1        |  |
| 227173_s_at         | -2.97620214103741 | 0               |                | BACH2       |  |
| 209619_at           | -2.86528990843459 | 0               |                | CD74        |  |
| 234660_s_at         | -2.81161728678359 | 0               |                | DIS3        |  |
| 202723_s_at         | -2.69572816449622 | 0               |                | FOXO1A      |  |
| 227700_x_at         | -2.59859831428636 | 0               |                | FLJ10709    |  |
| 219202_at           | -2.52442131777509 | 0               |                | FLJ22341    |  |
| 204638_at           | -2.51835721417786 | 0               |                | ACP5        |  |
| 222147_s_at         | -2.47042047428454 | 0               |                |             |  |
| 213772_s_at         | -2.41552637854988 | 0               |                | GGA2        |  |
| 203932_at           | -2.39804753895984 | 0               |                | HLA-DMB     |  |
| 205145_s_at         | -2.34102992713809 | 0               |                | MYL5        |  |
| 221969_at           | -2.278395672233   | 0.01            |                | PAX5        |  |
| 217521_at           | 2.26710710056045  | 0               |                |             |  |
| 205541_s_at         | -2.22303735713359 | 0               |                | GSPT2       |  |
| 204661_at           | -2.15814023268535 | 0               |                | CDW52       |  |
| 242729_at           | 2.02602724250151  | 0               |                |             |  |

|                             |                        |                 |                       |                    |
|-----------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>CML vs. ALL B not Ph</b> |                        | samples: 14 / 9 |                       |                    |
| accuracy                    | 1                      |                 |                       |                    |
| confidence                  | 1                      |                 |                       |                    |
| <b>gene</b>                 | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 206440_at                   | 3.54851691296324       | 0*              | 69.75                 | VELL1              |
| 223839_s_at                 | 2.95162251991881       | 0               |                       |                    |
| 201482_at                   | 2.5967465282815        | 0               |                       | QSCN6              |
| 223246_s_at                 | -2.53289104519377      | 0               |                       | STRBP              |
| 202477_s_at                 | -2.36949525800043      | 0               |                       | GCP2               |
| 227415_at                   | -2.35663515228965      | 0               |                       |                    |
| 202819_s_at                 | -2.31208048847973      | 0               |                       | TCEB3              |
| 226876_at                   | 2.29929647597952       | 0               |                       |                    |
| 200654_at                   | 2.2916645921996        | 0               |                       | P4HB               |
| 231472_at                   | -2.27133126588153      | 0               |                       |                    |
| 217521_at                   | 2.26710710056045       | 0               |                       |                    |
| 218764_at                   | -2.26149206068996      | 0               |                       | MGC5363            |
| 219615_s_at                 | 2.21717677908473       | 0               |                       | KCNK5              |
| 219111_s_at                 | -2.20588673666352      | 0               |                       | MGC2835            |
| 212268_at                   | 2.20005764504112       | 0               |                       | SERPINB1           |
| 211275_s_at                 | 2.1595066613388        | 0               |                       | GYG                |
| 211990_at                   | -2.15004013194548      | 0               |                       | HLA-DPA1           |
| 206676_at                   | 2.13116752502457       | 0               |                       | CEACAM8            |
| 235818_at                   | 2.13111499669481       | 0               |                       |                    |
| 210254_at                   | 2.07581294141343       | 0               |                       |                    |

|                       |                        |                  |                       |                    |
|-----------------------|------------------------|------------------|-----------------------|--------------------|
| <b>CML vs. ALL Ph</b> |                        | samples: 14 / 15 |                       |                    |
| accuracy              | 1                      |                  |                       |                    |
| confidence            | 1                      |                  |                       |                    |
| <b>gene</b>           | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 209619_at             | -3.47132181247921      | 0*               | 5777.85               | CD74               |
| 212778_at             | -3.09966497846595      | 0                |                       | KIAA0602           |
| 201029_s_at           | -3.08460906542498      | 0                |                       | MIC2               |
| 214317_x_at           | -3.02953000176234      | 0                |                       | RPS9               |
| 202332_at             | -2.9539112535883       | 0                |                       | CSNK1E             |
| 211990_at             | -2.80086525597245      | 0                |                       | HLA-DPA1           |
| 203373_at             | -2.76056827822619      | 0                |                       | STAT12             |
| 210487_at             | -2.66400596339357      | 0                |                       | DNTT               |
| 226844_at             | -2.53578669067924      | 0                |                       |                    |
| 207971_s_at           | -2.4877090389281       | 0                |                       | KIAA0582           |
| 206440_at             | 2.45272667930868       | 0                |                       | VELI1              |
| 205513_at             | 2.38968722893052       | 0                |                       | TCN1               |
| 211275_s_at           | 2.33552678870234       | 0                |                       | GYG                |
| 204670_x_at           | -2.32905695313267      | 0                |                       | HLA-DRB5           |
| 205557_at             | 2.3286749741246        | 0                |                       | BPI                |
| 220000_at             | 2.32132983989275       | 0                |                       | SIGLEC5            |
| 212531_at             | 2.31169568945083       | 0                |                       | LCN2               |
| 204174_at             | 2.3066969794321        | 0                |                       | ALOX5AP            |
| 225386_s_at           | 2.25229241478444       | 0                |                       | LOC92906           |
| 206111_at             | 2.22277368410809       | 0                |                       | RNASE2             |

**CML vs. T-ALL**

samples: 14 / 9

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 210254_at   | 4.72390509810889  | 0* | 3562.85        |             |
| 206111_at   | 4.12411957901486  | 0  |                | RNASE2      |
| 205557_at   | 4.12268252311326  | 0  |                | BPI         |
| 216379_x_at | 4.09576684675689  | 0  |                |             |
| 209771_x_at | 4.04268115620178  | 0  |                | CD24        |
| 204484_at   | -3.92079658637056 | 0  |                | PIK3C2B     |
| 203949_at   | 3.82080923209307  | 0  |                | MPO         |
| 206871_at   | 3.79666500221894  | 0  |                | ELA2        |
| 212268_at   | 3.66762573362107  | 0  |                | SERPINB1    |
| 239071_at   | -3.65785660037409 | 0  |                |             |
| 209772_s_at | 3.61720812003475  | 0  |                | CD24        |
| 212531_at   | 3.55056769994448  | 0  |                | LCN2        |
| 206440_at   | 3.54851691296324  | 0  |                | VELI1       |
| 242292_at   | -3.53231266693437 | 0  |                |             |
| 206676_at   | 3.51041964854693  | 0  |                | CEACAM8     |
| 218224_at   | -3.28568428621792 | 0  |                | PNMA1       |
| 211657_at   | 3.27814094785335  | 0  |                |             |
| 231215_at   | -3.27770330337019 | 0  |                |             |
| 211275_s_at | 3.26113496045954  | 0  |                | GYG         |
| 203757_s_at | 3.16440848129156  | 0  |                | CEACAM6     |

|                        |                        |          |                       |                    |
|------------------------|------------------------|----------|-----------------------|--------------------|
| <b>CML vs. AML +8</b>  | samples: 14 / 10       |          |                       |                    |
| accuracy               | 1                      |          |                       |                    |
| confidence             | 1                      |          |                       |                    |
| <b>gene</b>            | <b>signal-to-noise</b> | <b>p</b> | <b>decision limit</b> | <b>gene symbol</b> |
| 212531_at              | 3.91758233758871       | 0*       | 6654.5                | LCN2               |
| 218151_x_at            | -3.61342068798238      | 0        |                       | FLJ11856           |
| 203188_at              | -2.49453997369644      | 0        |                       | B3GNT6             |
| 225014_at              | -2.46286744087574      | 0        |                       |                    |
| 223894_s_at            | 2.42404553998791       | 0        |                       | FTS                |
| 227999_at              | -2.41422896946156      | 0        |                       | LOC170394          |
| 210244_at              | 2.30650676975445       | 0        |                       | CAMP               |
| 223226_x_at            | -2.1556086960975       | 0        |                       | MGC3181            |
| 205849_s_at            | -2.15471806280279      | 0        |                       | UQCRB              |
| 203936_s_at            | 2.12656987689311       | 0        |                       | MMP9               |
| 202080_s_at            | -2.08086044698338      | 0        |                       | KIAA1042           |
| 212146_at              | -2.00720003739628      | 0        |                       | KIAA0842           |
| 210749_x_at            | -2.00702022115248      | 0        |                       | DDR1               |
| 220755_s_at            | -1.97451125809376      | 0        |                       |                    |
| 211743_s_at            | 1.88718047009153       | 0        |                       | PRG2               |
| 214317_x_at            | -1.86316203101213      | 0        |                       | RPS9               |
| 214475_x_at            | 1.8601686492104        | 0        |                       | CAPN3              |
| 200094_s_at - HG-U133A | -1.83127854302456      | 0        |                       | EEF2               |
| 223939_at              | 1.81572736683912       | 0        |                       | GPR91              |
| 229934_at              | 1.65483415989943       | 0        |                       |                    |



**CML vs. AML complex**

samples: 14 / 36

accuracy

0.98

confidence

1

failed:

19

| gene        | signal-to-noise   | p  | decision limit | gene symbol   |
|-------------|-------------------|----|----------------|---------------|
| 209772_s_at | 2.25515756155772  | 0  | 10028.8        | CD24          |
| 212531_at   | 2.16780856655461  | 0* |                | LCN2          |
| 210244_at   | 2.05958595591104  | 0  |                | CAMP          |
| 205557_at   | 1.88114022725824  | 0  |                | BPI           |
| 207802_at   | 1.84224616530014  | 0  |                | SGP28         |
| 203936_s_at | 1.83245146841284  | 0  |                | MMP9          |
| 206676_at   | 1.82688412686061  | 0  |                | CEACAM8       |
| 216379_x_at | 1.82175067686641  | 0  |                |               |
| 209771_x_at | 1.71430561727442  | 0  |                | CD24          |
| 202265_at   | -1.71011447772371 | 0  |                | BMI1          |
| 209186_at   | -1.65481819707492 | 0  |                | ATP2A2        |
| 201029_s_at | -1.6407978740451  | 0  |                | MIC2          |
| 206440_at   | 1.62023824679434  | 0  |                | VELL1         |
| 218144_s_at | -1.60220955278722 | 0  |                | FLJ22056      |
| 212783_at   | -1.60173956589805 | 0  |                | DKFZp761B2423 |
| 225065_x_at | 1.5634162479603   | 0  |                |               |
| 214317_x_at | -1.51909514839257 | 0  |                | RPS9          |
| 212232_at   | -1.51499149327941 | 0  |                | KIAA1014      |
| 223894_s_at | 1.50378092313755  | 0  |                | FTS           |
| 207269_at   | 1.49292374711871  | 0  |                | DEFA4         |

|                           |                         |          |                       |                    |
|---------------------------|-------------------------|----------|-----------------------|--------------------|
| <b>CML vs. AML normal</b> | <b>samples: 14 / 62</b> |          |                       |                    |
| accuracy                  | 1                       |          |                       |                    |
| confidence                | 1                       |          |                       |                    |
| <b>gene</b>               | <b>signal-to-noise</b>  | <b>p</b> | <b>decision limit</b> | <b>gene symbol</b> |
| 212531_at                 | 3.52937454592387        | 0*       | 9007.35               | LCN2               |
| 209772_s_at               | 2.62224687740926        | 0        |                       | CD24               |
| 207802_at                 | 2.60464949585023        | 0        |                       | SGP28              |
| 205557_at                 | 2.59981269961356        | 0        |                       | BPI                |
| 206676_at                 | 2.51996784029752        | 0        |                       | CEACAM8            |
| 205513_at                 | 2.39713364221477        | 0        |                       | TCN1               |
| 209771_x_at               | 2.3694290541236         | 0        |                       | CD24               |
| 216379_x_at               | 2.36313392615064        | 0        |                       |                    |
| 211657_at                 | 2.35374478763084        | 0        |                       |                    |
| 203757_s_at               | 2.29281876629007        | 0        |                       | CEACAM6            |
| 202018_s_at               | 2.19711362051377        | 0        |                       | LTF                |
| 210254_at                 | 2.16927497946765        | 0        |                       |                    |
| 203021_at                 | 2.12970551783084        | 0        |                       | SLPI               |
| 205863_at                 | 2.10812748771569        | 0        |                       | S100A12            |
| 203936_s_at               | 2.07272259731953        | 0        |                       | MMP9               |
| 210244_at                 | 2.03624546792529        | 0        |                       | CAMP               |
| 204351_at                 | 2.0071543551955         | 0        |                       | S100P              |
| 211275_s_at               | 1.97937290056753        | 0        |                       | GYG                |
| 224967_at                 | 1.96229148265436        | 0        |                       |                    |
| 223894_s_at               | 1.92953251923329        | 0        |                       | FTS                |

CML vs. AML t(8;21)

samples: 14 / 13

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol  |
|-------------|-------------------|----|----------------|--------------|
| 207802_at   | 2.83774385104531  | 0  |                | SGP28        |
| 201425_at   | 2.50825834074572  | 0  |                | ALDH2        |
| 201029_s_at | -2.22223571455337 | 0* | 3078.2         | MIC2         |
| 205653_at   | 2.20106889451589  | 0  |                | CTSG         |
| 202391_at   | 2.10168460148023  | 0  |                | BASP1        |
| 209619_at   | -2.0547003400447  | 0  |                | CD74         |
| 228827_at   | -2.03460798747208 | 0  |                |              |
| 204670_x_at | -1.98893997185408 | 0  |                | HLA-DRB5     |
| 212531_at   | 1.96994267101106  | 0  |                | LCN2         |
| 203936_s_at | 1.92996861752981  | 0  |                | MMP9         |
| 225386_s_at | 1.90963950502737  | 0  |                | LOC92906     |
| 226878_at   | -1.90647418854412 | 0  |                |              |
| 201015_s_at | -1.90408812555782 | 0  |                | JUP          |
| 201281_at   | -1.88812152152812 | 0  |                | ADRM1        |
| 210982_s_at | -1.87330616648773 | 0  |                | HLA-DRA      |
| 210254_at   | 1.87025014628174  | 0  |                |              |
| 201137_s_at | -1.84763478416102 | 0  |                | HLA-DPB1     |
| 202545_at   | 1.81501795739179  | 0  |                | PRKCD        |
| 228485_s_at | 1.81223837093458  | 0  |                | CDW92        |
| 231969_at   | 1.61927333154015  | 0  |                | DKFZp762K222 |

| normal BM vs. all other |                   | samples: 9 / 260  |                |             |
|-------------------------|-------------------|-------------------|----------------|-------------|
| accuracy                |                   | 0.970260223048327 |                |             |
| confidence              |                   | 1                 |                |             |
| failed:                 |                   | 1,3,4,5,7,8,9,234 |                |             |
| gene                    | signal-to-noise   | p                 | decision limit | gene symbol |
| 202018_s_at             | 1.70014923965644  | 0                 |                | LTF         |
| 231241_at               | 1.68875870396623  | 0                 |                |             |
| 212531_at               | 1.61671894194992  | 0                 |                | LCN2        |
| 210244_at               | 1.4725412229519   | 0                 |                | CAMP        |
| 244652_at               | 1.41007652726897  | 0                 |                |             |
| 218916_at               | -1.40959768522889 | 0                 |                | FLJ23436    |
| 208141_s_at             | -1.39496085050899 | 0                 |                | MGC4293     |
| 218516_s_at             | -1.39489208362807 | 0                 |                | FLJ20421    |
| 224976_at               | 1.38035857849962  | 0                 |                | NFIA        |
| 201396_s_at             | -1.35501592670165 | 0                 |                | SGT         |
| 230988_at               | 1.27806474591682  | 0                 |                |             |
| 200631_s_at             | -1.27257367942543 | 0                 |                | SET         |
| 224975_at               | 1.25475272090295  | 0                 |                | NFIA        |
| 203535_at               | 1.24698765220296  | 0                 |                | S100A9      |
| 227497_at               | 1.24053728574653  | 0*                | 317.95         |             |
| 225792_at               | 1.2371690464102   | 0                 |                |             |
| 203367_at               | -1.23177778244874 | 0                 |                | DUSP14      |
| 40189_at                | -1.22367056036721 | 0                 |                | SET         |
| 225700_at               | 1.22315772266762  | 0                 |                |             |
| 223785_at               | 1.22097206282821  | 0                 |                | FLJ10719    |

| normal BM vs. ALL t(8;14) |                   | samples: 9 / 4 |                |             |  |
|---------------------------|-------------------|----------------|----------------|-------------|--|
| accuracy                  | 1                 |                |                |             |  |
| confidence                | 1                 |                |                |             |  |
| gene                      | signal-to-noise   | p              | decision limit | gene symbol |  |
| 222147_s_at               | -5.80632286389653 | 0*             | 48.2           |             |  |
| 209380_s_at               | 4.30105342509009  | 0              |                | ABCC5       |  |
| 230988_at                 | 4.0486666186669   | 0              |                |             |  |
| 227230_s_at               | 3.69195069014622  | 0              |                | KIAA1211    |  |
| 201278_at                 | 3.59730622800604  | 0              |                | DAB2        |  |
| 205051_s_at               | 3.55673529468534  | 0              |                | KIT         |  |
| 214558_at                 | 3.49255759470258  | 0              |                | GPR12       |  |
| 201988_s_at               | 3.46251302734757  | 0              |                | CREBL2      |  |
| 223253_at                 | 3.45322097101822  | 0              |                | UCC1        |  |
| 204285_s_at               | -3.35570555370453 | 0              |                | PMAIP1      |  |
| 237006_at                 | 3.14219078440997  | 0              |                |             |  |
| 217047_s_at               | 3.00448756016945  | 0              |                |             |  |
| 243020_at                 | 2.97861252444615  | 0              |                |             |  |
| 205690_s_at               | -2.97763156027721 | 0              |                | G10         |  |
| 234764_x_at               | 2.9597816169315   | 0              |                |             |  |
| 209160_at                 | 2.88288854646291  | 0.01           |                | AKR1C3      |  |
| 239835_at                 | -2.82125904680112 | 0              |                | KIAA1842    |  |
| 242434_at                 | -2.60351764410894 | 0.01           |                |             |  |
| 228708_at                 | 2.60104548908002  | 0.01           |                |             |  |
| 229575_at                 | 2.59826531472399  | 0              |                |             |  |

| normal BM vs. ALL B not Ph |                   | samples: 9 / 9 |                |             |
|----------------------------|-------------------|----------------|----------------|-------------|
| accuracy                   | 1                 |                |                |             |
| confidence                 | 1                 |                |                |             |
| gene                       | signal-to-noise   | p              | decision limit | gene symbol |
| 201506_at                  | 3.72288560994884  | 0*             | 464.35         | TGFB1       |
| 218718_at                  | 3.24294310152425  | 0              |                | PDGFC       |
| 205051_s_at                | 3.03451031560789  | 0              |                | KIT         |
| 235818_at                  | 2.5546546541523   | 0              |                |             |
| 202382_s_at                | 2.39296453276424  | 0              |                | GNPI        |
| 221802_s_at                | 2.32414568373485  | 0              |                | KIAA1598    |
| 238066_at                  | 2.17647785634866  | 0              |                | RBP7        |
| 203645_s_at                | 2.13814112768782  | 0              |                | CD163       |
| 227038_at                  | 2.09057615422001  | 0              |                |             |
| 225792_at                  | 2.07680085776485  | 0              |                |             |
| 202729_s_at                | 2.04654552970378  | 0              |                | LTBP1       |
| 230441_at                  | -2.03717805375485 | 0              |                |             |
| 212989_at                  | 2.00592033097705  | 0              |                |             |
| 201462_at                  | 1.98840399134665  | 0              |                | KIAA0193    |
| 227627_at                  | 1.97570787395888  | 0              |                | SGKL        |
| 204112_s_at                | 1.90974025156521  | 0              |                | HNMT        |
| 204285_s_at                | -1.90604496284052 | 0              |                | PMAIP1      |
| 223044_at                  | 1.88064158446644  | 0              |                | SLC11A3     |
| 223839_s_at                | 1.86406616667336  | 0              |                |             |
| 204225_at                  | 1.85888952621093  | 0              |                | HDAC4       |

| normal BM vs. ALL Ph |                   | samples: 9 / 15 |                |               |
|----------------------|-------------------|-----------------|----------------|---------------|
| accuracy             | 1                 |                 |                |               |
| confidence           | 1                 |                 |                |               |
| gene                 | signal-to-noise   | p               | decision limit | gene symbol   |
| 225792_at            | 5.04037264761662  | 0*              | 76.45          |               |
| 224976_at            | 4.534006778733    | 0               |                | NFIA          |
| 227230_s_at          | 3.69195069014622  | 0               |                | KIAA1211      |
| 203373_at            | -3.60116056485263 | 0               |                | STAT12        |
| 202332_at            | -3.19705046805115 | 0               |                | CSNK1E        |
| 212778_at            | -3.09966497846595 | 0               |                | KIAA0602      |
| 230988_at            | 3.03359562676407  | 0               |                |               |
| 218718_at            | 3.0129378014466   | 0               |                | PDGFC         |
| 205624_at            | 2.79751505147013  | 0               |                | CPA3          |
| 224975_at            | 2.78377945957649  | 0               |                | NFIA          |
| 234107_s_at          | 2.7482082597836   | 0               |                |               |
| 217988_at            | -2.7439427550045  | 0               |                | HEI10         |
| 202945_at            | -2.67000372671022 | 0               |                | FPGS          |
| 218916_at            | -2.6636521234692  | 0               |                | FLJ23436      |
| 223044_at            | 2.59882500535427  | 0               |                | SLC11A3       |
| 226751_at            | 2.41273912703748  | 0               |                | DKFZP566K1924 |
| 210487_at            | -2.38376037071424 | 0               |                | DNTT          |
| 201029_s_at          | -2.37712949687212 | 0               |                | MIC2          |
| 207971_s_at          | -2.36738543730614 | 0               |                | KIAA0582      |
| 203645_s_at          | 2.32470988727879  | 0               |                | CD163         |

|                            |                        |                       |                       |                    |
|----------------------------|------------------------|-----------------------|-----------------------|--------------------|
| <b>normal BM vs. T-ALL</b> |                        | <b>samples: 9 / 9</b> |                       |                    |
| accuracy                   | 1                      |                       |                       |                    |
| confidence                 | 1                      |                       |                       |                    |
| <b>gene</b>                | <b>signal-to-noise</b> | <b>p</b>              | <b>decision limit</b> | <b>gene symbol</b> |
| 231241_at                  | 5.25713497545753       | 0*                    | 52.3                  |                    |
| 225792_at                  | 5.04037264761662       | 0                     |                       |                    |
| 224976_at                  | 4.534006778733         | 0                     |                       | NFIA               |
| 204484_at                  | -3.92079658637056      | 0                     |                       | PIK3C2B            |
| 218516_s_at                | -3.89821124480393      | 0.01                  |                       | FLJ20421           |
| 244652_at                  | 3.8571916430704        | 0                     |                       |                    |
| 210613_s_at                | 3.6441364713354        | 0                     |                       | SYNGR1             |
| 206488_s_at                | 3.59792987181253       | 0                     |                       | CD36               |
| 201416_at                  | -3.57631738716755      | 0                     |                       | SOX4               |
| 201417_at                  | -3.57222567838335      | 0                     |                       |                    |
| 218224_at                  | -3.56533208466192      | 0                     |                       | PNMA1              |
| 206871_at                  | 3.49320660549908       | 0                     |                       | ELA2               |
| 214575_s_at                | 3.38517251606938       | 0                     |                       | AZU1               |
| 221188_s_at                | 3.26852421442154       | 0                     |                       | CIDEB              |
| 203104_at                  | 3.11161266045758       | 0                     |                       | CSF1R              |
| 226190_at                  | 3.08925054797494       | 0                     |                       |                    |
| 202018_s_at                | 3.06471974822162       | 0                     |                       | LTF                |
| 200631_s_at                | -3.05905666007645      | 0                     |                       | SET                |
| 224970_at                  | 3.05809311507561       | 0                     |                       | NFIA               |
| 212531_at                  | 3.03461908631694       | 0                     |                       | LCN2               |



|                      |                   |                 |                |             |  |
|----------------------|-------------------|-----------------|----------------|-------------|--|
| normal BM vs. AML +8 |                   | samples: 9 / 10 |                |             |  |
| accuracy             | 1                 |                 |                |             |  |
| confidence           | 1                 |                 |                |             |  |
| gene                 | signal-to-noise   | p               | decision limit | gene symbol |  |
| 231241_at            | 5.25713497545753  | 0*              | 52.3           |             |  |
| 218916_at            | -4.40926777727725 | 0               |                | FLJ23436    |  |
| 218151_x_at          | -3.61342068798238 | 0               |                | FLJ11856    |  |
| 212531_at            | 3.35638912536087  | 0               |                | LCN2        |  |
| 225014_at            | -2.46286744087574 | 0               |                |             |  |
| 210244_at            | 2.4347108722936   | 0               |                | CAMP        |  |
| 227999_at            | -2.41422896946156 | 0               |                | LOC170394   |  |
| 220755_s_at          | -2.40201593179233 | 0               |                |             |  |
| 202945_at            | -2.37212917164108 | 0               |                | FPGS        |  |
| 214109_at            | 2.28939588941522  | 0               |                | LRBA        |  |
| 225792_at            | 2.20832306168575  | 0               |                |             |  |
| 238066_at            | 2.17647785634866  | 0               |                | RBP7        |  |
| 217179_x_at          | 2.173252865121    | 0               |                |             |  |
| 200631_s_at          | -2.1126574466818  | 0               |                | SET         |  |
| 234764_x_at          | 2.11173306630787  | 0               |                |             |  |
| 225547_at            | -2.10764119746987 | 0               |                |             |  |
| 205849_s_at          | -2.04438654979845 | 0               |                | UQCRB       |  |
| 208141_s_at          | -2.04344739454244 | 0               |                | MGC4293     |  |
| 233613_x_at          | 2.02519262390017  | 0               |                |             |  |

|                                  |                        |                 |                       |                    |
|----------------------------------|------------------------|-----------------|-----------------------|--------------------|
| <b>normal BM vs. AML complex</b> |                        | samples: 9 / 36 |                       |                    |
| accuracy                         | 0.9777777777777778     |                 |                       |                    |
| confidence                       | 1                      |                 |                       |                    |
| failed:                          | 15                     |                 |                       |                    |
| <b>gene</b>                      | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |
| 231241_at                        | 2.20113810647196       | 0*              | 94.5                  |                    |
| 210244_at                        | 2.15797898100991       | 0               |                       | CAMP               |
| 226734_at                        | 2.10647394623844       | 0               |                       |                    |
| 218516_s_at                      | -2.0003648205556       | 0               |                       | FLJ20421           |
| 244652_at                        | 1.9350839662771        | 0               |                       |                    |
| 201595_s_at                      | -1.81799799553143      | 0               |                       | HT010              |
| 212531_at                        | 1.80637620431712       | 0               |                       | LCN2               |
| 201396_s_at                      | -1.79606593499252      | 0               |                       | SGT                |
| 203092_at                        | -1.77664454556306      | 0               |                       | TIMM44             |
| 230795_at                        | -1.75873906279717      | 0               |                       | H4F2               |
| 228377_at                        | 1.70396224015785       | 0               |                       | KIAA1384           |
| 208141_s_at                      | -1.66429492261381      | 0               |                       | MGC4293            |
| 202265_at                        | -1.62376492554641      | 0               |                       | BMI1               |
| 202018_s_at                      | 1.60476985758804       | 0               |                       | LTF                |
| 218916_at                        | -1.58708293547372      | 0               |                       | FLJ23436           |
| 224406_s_at                      | 1.57633156642315       | 0               |                       | IRTA2              |
| 209806_at                        | -1.57424329592102      | 0               |                       | H2B/S              |
| 208645_s_at                      | 1.5695109709269        | 0               |                       |                    |
| 200040_at - HG-U133A             | -1.548128254162        | 0               |                       | KHDRBS1            |
| AFFX-HSAC07/X00351_M_at -        |                        |                 |                       |                    |
| HG-U133A                         | 1.11476993738169       | 0               |                       | ACTB               |

|                          |                   |                 |                |             |
|--------------------------|-------------------|-----------------|----------------|-------------|
| normal BM vs. AML normal |                   | samples: 9 / 62 |                |             |
| accuracy                 | 1                 |                 |                |             |
| confidence               | 1                 |                 |                |             |
| gene                     | signal-to-noise   | p               | decision limit | gene symbol |
| 212531_at                | 3.03296310695958  | 0*              | 8390.45        | LCN2        |
| 202018_s_at              | 2.55569861815605  | 0               |                | LTF         |
| 210244_at                | 2.12911144557531  | 0               |                | CAMP        |
| 231241_at                | 1.90756814920388  | 0               |                |             |
| 234764_x_at              | 1.88445719282136  | 0               |                |             |
| 238066_at                | 1.84490304262637  | 0               |                | RBP7        |
| 218516_s_at              | -1.76767038599239 | 0               |                | FLJ20421    |
| 214651_s_at              | -1.75409579509524 | 0               |                | HOXA9       |
| 207802_at                | 1.69982859144728  | 0               |                | SGP28       |
| 203535_at                | 1.6861966835666   | 0               |                | S100A9      |
| 224976_at                | 1.68580070345942  | 0               |                | NFIA        |
| 235818_at                | 1.65829753113564  | 0               |                |             |
| 226188_at                | 1.63500287325021  | 0               |                |             |
| 208651_x_at              | 1.6330531805719   | 0               |                | CD24        |
| 214523_at                | 1.61056786968333  | 0               |                | CEBPE       |
| 206871_at                | 1.60161598002874  | 0               |                | ELA2        |
| 224970_at                | 1.57809657249869  | 0               |                | NFIA        |
| 210004_at                | 1.57705611671231  | 0               |                | OLR1        |
| 208141_s_at              | -1.55515435811455 | 0               |                | MGC4293     |
| 215379_x_at              | 1.53008885935316  | 0               |                | IGLJ3       |

|                           |                  |                 |                |             |
|---------------------------|------------------|-----------------|----------------|-------------|
| normal BM vs. AML t{8;21} |                  | samples: 9 / 13 |                |             |
| accuracy                  | 1                |                 |                |             |
| confidence                | 1                |                 |                |             |
| gene                      | signal-to-noise  | p               | decision limit | gene symbol |
| 225792_at                 | 5.04037264761662 | 0*              | 76.45          |             |
| 224976_at                 | 4.534006778733   | 0               |                | NFIA        |
| 201425_at                 | 3.96306688659586 | 0               |                | ALDH2       |
| 201506_at                 | 3.72288560994884 | 0               |                | TGFB1       |
| 208146_s_at               | 3.28524851571637 | 0               |                | CPVL        |
| 224970_at                 | 3.05809311507561 | 0               |                | NFIA        |
| 206488_s_at               | 2.8751017477522  | 0               |                | CD36        |
| 226818_at                 | 2.67802773991406 | 0               |                |             |
| 224975_at                 | 2.55138740597295 | 0               |                | NFIA        |
| 227388_at                 | 2.49815087819486 | 0               |                |             |
| 217963_s_at               | 2.48471435523086 | 0               |                | HCS         |
| 233613_x_at               | 2.45189729191801 | 0               |                |             |
| 228766_at                 | 2.45082385023982 | 0               |                |             |
| 208908_s_at               | 2.41879730006023 | 0               |                | CAST        |
| 212586_at                 | 2.33228373164484 | 0               |                | ARTS-1      |
| 221802_s_at               | 2.32414568373485 | 0               |                | KIAA1598    |
| 224823_at                 | 2.30113027005505 | 0               |                |             |
| 213624_at                 | 2.29634946162627 | 0               |                | ASM3A       |
| 221731_x_at               | 2.26796857130761 | 0               |                | CSPG2       |
| 225426_at                 | 2.26611296861875 | 0               |                |             |

ALL t(8;14) vs. ALL Ph

samples: 4 / 15

accuracy

1

confidence

1

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 204663_at   | -3.923285216392   | 0* | 80.55          | ME3         |
| 203373_at   | -3.79361888147031 | 0  |                | STAT12      |
| 207971_s_at | -3.75632756767036 | 0  |                | KIAA0582    |
| 221834_at   | -3.73210732395713 | 0  |                |             |
| 212535_at   | -3.35180803492209 | 0  |                |             |
| 210487_at   | -2.66400596339357 | 0  |                | DNTT        |
| 226607_at   | -2.65303285070543 | 0  |                | L3MBTL      |
| 214505_s_at | -2.30002142127038 | 0  |                | FHL1        |
| 226545_at   | -2.26350222846019 | 0  |                |             |
| 201540_at   | -2.21889045310099 | 0  |                | FHL1        |
| 209253_at   | -2.17983750831107 | 0  |                | SCAM-1      |
| 228496_s_at | -2.17784383479245 | 0  |                | CRIM1       |
| 213854_at   | -2.14963630962421 | 0  |                | SYNGR1      |
| 228211_at   | -2.14770747938169 | 0  |                |             |
| 212012_at   | -2.10857376713896 | 0  |                | D2S448      |
| 208217_at   | -2.10769716540219 | 0  |                | GABRR2      |
| 202519_at   | -2.0579870997007  | 0  |                | MONDOA      |
| 218836_at   | 2.05747195088222  | 0  |                | FLJ22638    |
| 211031_s_at | -2.05686503189171 | 0  |                | CYLN2       |
| 50277_at    | 1.4804958933411   | 0  |                | GGA1        |

| ALL t(8;14) vs. T-ALL |                   | samples: 4 / 9 |                |             |  |
|-----------------------|-------------------|----------------|----------------|-------------|--|
| accuracy              | 1                 |                |                |             |  |
| confidence            | 1                 |                |                |             |  |
| gene                  | signal-to-noise   | p              | decision limit | gene symbol |  |
| 213772_s_at           | 4.99941703918842  | 0*             | 105.35         | GGA2        |  |
| 236019_at             | -4.8835710129593  | 0              |                |             |  |
| 225277_at             | -4.63399536600695 | 0              |                |             |  |
| 40148_at              | 3.56542456382539  | 0              |                | APBB2       |  |
| 228211_at             | -3.35861431980337 | 0              |                |             |  |
| 201334_s_at           | 3.32612092220108  | 0              |                | ARHGEF12    |  |
| 201417_at             | -2.74359054965603 | 0              |                |             |  |
| 206241_at             | -2.66958809534806 | 0              |                | KPNA5       |  |
| 208918_s_at           | 2.59071326340578  | 0              |                | FLJ13052    |  |
| 210038_at             | -2.55792113825771 | 0              |                |             |  |
| 225735_at             | -2.54773299400117 | 0              |                |             |  |
| 209253_at             | -2.33749346955264 | 0              |                | SCAM-1      |  |
| 202262_x_at           | -2.29867528817227 | 0              |                | DDAH2       |  |
| 225129_at             | 2.29232308514395  | 0              |                | MDS026      |  |
| 221969_at             | 2.278395672233    | 0              |                | PAX5        |  |
| 225080_at             | 2.24115131588386  | 0              |                | MYO1C       |  |
| 218338_at             | -2.22116851483018 | 0              |                | EDR1        |  |
| 208664_s_at           | -2.20362132175544 | 0              |                | TTC3        |  |
| 201029_s_at           | -2.14618908100153 | 0.01           |                | MIC2        |  |
| 56256_at              | 1.43796973813133  | 0              |                | LOC51092    |  |

ALL t(8;14) vs. AML +8

samples: 4 / 10

accuracy

1

confidence

1

| gene        | signal-to-noise   | p    | decision limit | gene symbol |
|-------------|-------------------|------|----------------|-------------|
| 213159_at   | -4.39324002240111 | 0*   | 42.05          | KIAA0805    |
| 226607_at   | -4.38967336864894 | 0    |                | L3MBTL      |
| 205420_at   | -3.4525752660757  | 0    |                | PEX7        |
| 202137_s_at | -3.07008892450809 | 0    |                | BS69        |
| 36004_at    | -2.57531929513625 | 0.01 |                | IKBKG       |
| 203731_s_at | -2.45523698701432 | 0    |                | ZFP95       |
| 212349_at   | -2.36608074328153 | 0    |                | POFUT1      |
| 209253_at   | -2.32838757070082 | 0.01 |                | SCAM-1      |
| 213238_at   | -2.28171034767303 | 0    |                | ATP10D      |
| 223382_s_at | -2.21844659554677 | 0    |                | NIN283      |
| 219291_at   | -2.18210292149327 | 0    |                | MDS009      |
| 212293_at   | -2.11981778828952 | 0    |                | KIAA0630    |
| 1729_at     | -1.99780531744703 | 0    |                | TRADD       |
| 225959_s_at | -1.99555471271853 | 0.01 |                | NIN283      |
| 205690_s_at | 1.97864646284407  | 0    |                | G10         |
| 243579_at   | 1.96429396023857  | 0    |                | MSI2        |
| 220564_at   | 1.95122068807877  | 0    |                | FLJ11218    |
| 210896_s_at | -1.94074678448131 | 0    |                | ASPH        |
| 221617_at   | -1.92262620134603 | 0.02 |                |             |

|                                    |                        |                 |                       |                    |  |
|------------------------------------|------------------------|-----------------|-----------------------|--------------------|--|
| <b>ALL t(8;14) vs. AML complex</b> |                        | samples: 4 / 36 |                       |                    |  |
| accuracy                           | 0.975                  |                 |                       |                    |  |
| confidence                         | 0.967090153309866      |                 |                       |                    |  |
| failed:                            | 4                      |                 |                       |                    |  |
| <b>gene</b>                        | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |  |
| 36004_at                           | -1.99819054416994      | 0               |                       | IKBKG              |  |
| 228410_at                          | -1.91203372111762      | 0               |                       | GAB3               |  |
| 226291_at                          | -1.85352930781754      | 0               |                       | ALS2               |  |
| 239478_x_at                        | -1.83892006057297      | 0               |                       |                    |  |
| 201278_at                          | -1.78640641972044      | 0               |                       | DAB2               |  |
| 213073_at                          | -1.78527733316412      | 0               |                       | KIAA0321           |  |
| 36920_at                           | -1.77637196930535      | 0               |                       | MTM1               |  |
| 237864_at                          | -1.75181406771053      | 0               |                       |                    |  |
| 206550_s_at                        | -1.74071643864686      | 0.01            |                       | NUP155             |  |
| 213779_at                          | -1.71354352282537      | 0               |                       |                    |  |
| 237006_at                          | -1.71319042514024      | 0               |                       |                    |  |
| 206847_s_at                        | -1.68023930751716      | 0               |                       | HOXA7              |  |
| 213639_s_at                        | -1.6794904444526       | 0               |                       | KIAA0557           |  |
| 40148_at                           | 1.6627909781575        | 0*              | 64                    | APBB2              |  |
| 210358_x_at                        | -1.62491966279342      | 0               |                       | MGC2306            |  |
| 205420_at                          | -1.62469403094415      | 0               |                       | PEX7               |  |
| 226499_at                          | -1.60847740357238      | 0               |                       |                    |  |
| 212293_at                          | -1.56783564141892      | 0*              | 524.25                | KIAA0630           |  |
| 228211_at                          | -1.5662932955074       | 0               |                       |                    |  |
| AFFX-r2-Hs28SrRNA-5_at             |                        |                 |                       |                    |  |
| HG-U133B                           | 0.804899059460234      | 0               |                       |                    |  |



|                                   |                        |                 |                       |                    |  |
|-----------------------------------|------------------------|-----------------|-----------------------|--------------------|--|
| <b>ALL t(8;14) vs. AML normal</b> |                        | samples: 4 / 62 |                       |                    |  |
| accuracy                          | 1                      |                 |                       |                    |  |
| confidence                        | 0.94492014468957       |                 |                       |                    |  |
| <b>gene</b>                       | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |  |
| 242774_at                         | 2.1771591988175        | 0               |                       | SYNE-2             |  |
| 226066_at                         | -2.1383489258559       | 0               |                       |                    |  |
| 239478_x_at                       | -1.86376314754514      | 0               |                       |                    |  |
| 40148_at                          | 1.78834322080621       | 0*              | 53.3                  | APBB2              |  |
| 214651_s_at                       | -1.72987407199338      | 0               |                       | HOXA9              |  |
| 241421_at                         | -1.69137753712694      | 0               |                       |                    |  |
| 225277_at                         | -1.68295316743627      | 0               |                       |                    |  |
| 237864_at                         | -1.66733222775185      | 0               |                       |                    |  |
| 231181_at                         | 1.63598703935064       | 0               |                       |                    |  |
| 227173_s_at                       | 1.58512628703822       | 0               |                       | BACH2              |  |
| 228410_at                         | -1.58118628637501      | 0               |                       | GAB3               |  |
| 226607_at                         | -1.56767039969117      | 0               |                       | L3MBTL             |  |
| 206398_s_at                       | 1.56041095418581       | 0               |                       | CD19               |  |
| 226590_at                         | -1.55939441513481      | 0.01            |                       |                    |  |
| 223391_at                         | 1.54577336325056       | 0               |                       | LOC81537           |  |
| 205420_at                         | -1.53228798256568      | 0               |                       | PEX7               |  |
| 240106_at                         | -1.53045374201368      | 0               |                       |                    |  |
| 236019_at                         | -1.50700230486984      | 0               |                       |                    |  |
| 214558_at                         | -1.50544788292166      | 0               |                       | GPR12              |  |
| AFFX-HUMRGE/M10098_3_at           |                        |                 |                       |                    |  |
| - HG-U133B                        | 0.698344697289208      | 0               |                       |                    |  |

|                             |                   |                 |                |             |  |
|-----------------------------|-------------------|-----------------|----------------|-------------|--|
| ALL t(8;14) vs. AML t(8;21) |                   | samples: 4 / 13 |                |             |  |
| accuracy                    | 1                 |                 |                |             |  |
| confidence                  | 1                 |                 |                |             |  |
| gene                        | signal-to-noise   | p               | decision limit | gene symbol |  |
| 40148_at                    | 3.56542456382539  | 0*              | 32.75          | APBB2       |  |
| 239835_at                   | 3.10722969539603  | 0               |                | KIAA1842    |  |
| 225277_at                   | -2.97531197185908 | 0               |                |             |  |
| 225306_s_at                 | -2.20761036808439 | 0               |                |             |  |
| 210664_s_at                 | -2.19905382124823 | 0               |                | TFPI        |  |
| 218319_at                   | 2.13133938217549  | 0               |                | PELI1       |  |
| 212985_at                   | 2.10403815234864  | 0               |                |             |  |
| 238155_at                   | 2.09456306072679  | 0               |                |             |  |
| 221617_at                   | -2.04115820286726 | 0               |                |             |  |
| 220307_at                   | -2.04090815318901 | 0               |                | CD244       |  |
| 225250_at                   | 2.04032419238326  | 0               |                | STIM2       |  |
| 217080_s_at                 | -2.03866301670049 | 0               |                | HOMER-2B    |  |
| 228827_at                   | -2.03460798747208 | 0               |                |             |  |
| 214558_at                   | -2.02268322634707 | 0.01            |                | GPR12       |  |
| 230650_at                   | -2.02205697080977 | 0               |                |             |  |
| 226546_at                   | -2.00802538838226 | 0               |                |             |  |
| 219478_at                   | -1.99876002437156 | 0               |                | WFDC1       |  |
| 211709_s_at                 | -1.99340446769437 | 0               |                | SCGF        |  |
| 219789_at                   | -1.96292007200438 | 0               |                | NPR3        |  |
| 231181_at                   | 1.9495774287402   | 0               |                |             |  |

## ALL B not Ph vs. all other

samples: 9 / 260

accuracy 0.988847583643123

confidence 0.749589637027985

failed: 1,2,8

| gene        | signal-to-noise    | p  | decision limit | gene symbol  |
|-------------|--------------------|----|----------------|--------------|
| 230441_at   | 1.31003692018591   | 0  |                |              |
| 202382_s_at | -1.16916758328947  | 0  |                | GNPI         |
| 229253_at   | -1.06515235605176  | 0  |                | CTMP         |
| 201482_at   | -1.03614111933273  | 0  |                | QSCN6        |
| 214116_at   | -1.00681323467099  | 0  |                | BTD          |
| 224435_at   | 0.992700829908313  | 0  |                | MGC4248      |
| 229344_x_at | 0.972107787450054  | 0  |                | KIAA1238     |
| 229487_at   | 0.965321723620396  | 0* | 1              |              |
| 217559_at   | 0.963455203763842  | 0  |                | RPL10L       |
| 212592_at   | 0.956367645094086  | 0* | 4436.6         |              |
| 209197_at   | 0.921039694411825  | 0* | 637.1          | KIAA0080     |
| 223469_at   | -0.914920276631408 | 0* | 1              | MGC10812     |
| 224739_at   | 0.904429749740017  | 0* | 1              | MG61         |
| 218351_at   | -0.898398261455524 | 0* | 145.5          | FLJ20502     |
| 220744_s_at | -0.893719737391747 | 0* | 1              | WDR10        |
| 213582_at   | -0.888860830483358 | 0* | 1              | ATP11A       |
| 219615_s_at | -0.8878326695192   | 0* | 1              | KCNK5        |
| 203795_s_at | 0.880543704938786  | 0  |                | BCL7A        |
| 229817_at   | 0.879488726239199  | 0  |                | DKFZP434M098 |
| 244876_at   | 0.877426806604064  | 0  |                |              |

**ALL B not Ph vs. ALL Ph**

samples: 9 / 15

accuracy 0.916666666666667

confidence 1

failed: 3,10

| gene        | signal-to-noise    | p    | decision limit | gene symbol |
|-------------|--------------------|------|----------------|-------------|
| 219358_s_at | -1.52735607926994  | 0    |                | CENTA2      |
| 241383_at   | -1.07499870203752  | 0.01 |                |             |
| 213895_at   | -1.05505220750298  | 0    |                | EMP1        |
| 202123_s_at | -1.02481061931947  | 0*   | 753.7          | ABL1        |
| 205911_at   | -1.0236634987836   | 0    |                | PTHR1       |
| 242223_at   | 1.02343172223498   | 0.01 |                |             |
| 211709_s_at | -1.01491744255679  | 0    |                | SCGF        |
| 234839_at   | -1.00185285072786  | 0    |                |             |
| 212150_at   | -0.996731200580515 | 0    |                | KIAA0143    |
| 221991_at   | -0.987741661696868 | 0    |                | NXPH3       |
| 218543_s_at | 0.973909033712243  | 0    |                | FLJ22693    |
| 201874_at   | 0.966766364385792  | 0    |                | FLJ21047    |
| 212188_at   | -0.947998533949464 | 0    |                | LOC115207   |
| 241810_at   | -0.944344027780102 | 0.01 |                |             |
| 207520_at   | -0.936622132674122 | 0    |                |             |
| 213979_s_at | -0.935519171149618 | 0    |                | CTBP1       |
| 229745_x_at | -0.93424475879621  | 0.01 |                |             |
| 216680_s_at | -0.934196756237652 | 0    |                | EPHB4       |
| 202572_s_at | 0.924395823520243  | 0    |                | KIAA0964    |
| 243228_at   | 0.916138491705783  | 0    |                |             |

|                               |                        |                |                       |                    |
|-------------------------------|------------------------|----------------|-----------------------|--------------------|
| <b>ALL B not Ph vs. T-ALL</b> |                        | samples: 9 / 9 |                       |                    |
| accuracy                      | 1                      |                |                       |                    |
| confidence                    | 1                      |                |                       |                    |
| <b>gene</b>                   | <b>signal-to-noise</b> | <b>p</b>       | <b>decision limit</b> | <b>gene symbol</b> |
| 242292_at                     | -3.53231266693437      | 0*             | 19.4                  |                    |
| 36566_at                      | 2.04687603382912       | 0              |                       | CTNS               |
| 230636_s_at                   | 1.96129371358941       | 0              |                       | BTEB1              |
| 266_s_at                      | 1.95685220231101       | 0              |                       | CD24               |
| 209771_x_at                   | 1.95325312023269       | 0              |                       | CD24               |
| 219631_at                     | -1.90940390225071      | 0              |                       | FLJ12929           |
| 202113_s_at                   | 1.86969444770264       | 0              |                       | SNX2               |
| 216379_x_at                   | 1.84446878357139       | 0              |                       |                    |
| 221969_at                     | 1.82924887172424       | 0              |                       | PAX5               |
| 229487_at                     | 1.78170685853126       | 0              |                       |                    |
| 208650_s_at                   | 1.77571318786079       | 0              |                       | CD24               |
| 218464_s_at                   | -1.71465707824422      | 0              |                       | FLJ10700           |
| 213944_x_at                   | 1.69297405468728       | 0              |                       |                    |
| 226496_at                     | 1.65125933296341       | 0              |                       |                    |
| 202206_at                     | -1.58502966518677      | 0              |                       | ARL7               |
| 205504_at                     | 1.58481348793145       | 0              |                       | BTK                |
| 213539_at                     | -1.56405807954932      | 0              |                       | CD3D               |
| 211101_x_at                   | 1.55958748994576       | 0.01           |                       | LILRA2             |
| 244876_at                     | 1.55727218904507       | 0              |                       |                    |
| 209772_s_at                   | 1.54041193817483       | 0              |                       | CD24               |

| ALL B not Ph vs. AML +8 |                   | samples: 9 / 10 |                |             |  |
|-------------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy                | 1                 |                 |                |             |  |
| confidence              | 1                 |                 |                |             |  |
| gene                    | signal-to-noise   | p               | decision limit | gene symbol |  |
| 229253_at               | -2.32958521030012 | 0               |                | CTMP        |  |
| 230441_at               | 2.03717805375485  | 0               |                |             |  |
| 202382_s_at             | -2.02017770346207 | 0               |                | GNPI        |  |
| 209135_at               | -1.93398721370049 | 0               |                | ASPH        |  |
| 229487_at               | 1.78170685853126  | 0               |                |             |  |
| 236656_s_at             | 1.74257382856431  | 0               |                |             |  |
| 206438_x_at             | -1.68325155133202 | 0               |                | FLJ12975    |  |
| 207403_at               | -1.66596170819766 | 0               |                | IRS4        |  |
| 219615_s_at             | -1.66280630807372 | 0               |                | KCNK5       |  |
| 51192_at                | -1.66236513015575 | 0               |                | SSH-3       |  |
| 208248_x_at             | -1.64870519570629 | 0*              | 1987.65        | APLP2       |  |
| 218109_s_at             | -1.60915618696108 | 0               |                | FLJ14153    |  |
| 206295_at               | -1.5980305395866  | 0               |                | IL18        |  |
| 219013_at               | -1.59551449458991 | 0               |                | FLJ21634    |  |
| 217979_at               | 1.59385936644152  | 0               |                | NET-6       |  |
| 208674_x_at             | -1.58849840915584 | 0               |                | DDOST       |  |
| 213474_at               | 1.58394324440508  | 0               |                |             |  |
| 218351_at               | -1.58117397105311 | 0               |                | FLJ20502    |  |
| 235422_at               | 1.57754106652849  | 0               |                | FALZ        |  |
| 227709_at               | 1.573035497361    | 0               |                | RCN1        |  |

**ALL B not Ph vs. AML****complex** samples: 9 / 36

accuracy 1

confidence 0.975685516889171

| gene        | signal-to-noise   | p    | decision limit | gene symbol |
|-------------|-------------------|------|----------------|-------------|
| 230441_at   | 2.03717805375485  | 0    |                |             |
| 218168_s_at | -1.58072460849855 | 0*   | 584.1          | CABC1       |
| 219615_s_at | -1.55121221944569 | 0    |                | KCNK5       |
| 200620_at   | -1.52004960803633 | 0    |                | C1orf8      |
| 229487_at   | 1.50364388130017  | 0    |                |             |
| 218718_at   | -1.4701929847603  | 0    |                | PDGFC       |
| 203372_s_at | 1.43481740588652  | 0    |                | STATI2      |
| 205997_at   | -1.40495787127453 | 0    |                | ADAM28      |
| 221969_at   | 1.3801763712428   | 0    |                | PAX5        |
| 209628_at   | -1.36215023734312 | 0    |                | P15-2       |
| 243362_s_at | 1.346548683162    | 0    |                | LEF1        |
| 219362_at   | -1.34586251735194 | 0    |                | FLJ22643    |
| 244876_at   | 1.32930450347737  | 0    |                |             |
| 227038_at   | -1.3285550634404  | 0    |                |             |
| 215001_s_at | -1.31302949268385 | 0    |                | GLUL        |
| 202382_s_at | -1.31028007399306 | 0    |                | GNPI        |
| 211574_s_at | -1.27970708025177 | 0    |                | MCP         |
| 203373_at   | 1.2683089746763   | 0    |                | STATI2      |
| 206847_s_at | -1.25861755739009 | 0    |                | HOXA7       |
| 90610_at    | 0.53320359867076  | 0.01 |                | LRRN1       |

ALL B not Ph vs. AML normal samples: 9 / 62

accuracy 0.985915492957746

confidence 1

failed: 51

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 230441_at   | 1.6244512124777   | 0  |                |             |
| 229487_at   | 1.5789226463723   | 0  |                |             |
| 244876_at   | 1.55727218904507  | 0  |                |             |
| 230659_at   | 1.54315361034532  | 0  |                | KIAA0212    |
| 214651_s_at | -1.46222218442109 | 0  |                | HOXA9       |
| 221969_at   | 1.45958458157821  | 0* | 695.5          | PAX5        |
| 222915_s_at | 1.43752454061174  | 0  |                | BANK        |
| 204215_at   | 1.3973053569742   | 0  |                | MGC4175     |
| 223469_at   | -1.39620868523075 | 0  |                | MGC10812    |
| 205997_at   | -1.3950951014202  | 0  |                | ADAM28      |
| 229253_at   | -1.35885129348099 | 0  |                | CTMP        |
| 209905_at   | -1.35690502004825 | 0  |                | HOXA9       |
| 236656_s_at | 1.33665521300451  | 0  |                |             |
| 205382_s_at | -1.33068263294683 | 0  |                | DF          |
| 214761_at   | 1.3284704024734   | 0  |                | OAZ         |
| 235753_at   | -1.3151317291794  | 0  |                |             |
| 218351_at   | -1.29563799307181 | 0  |                | FLJ20502    |
| 243362_s_at | 1.29364059417566  | 0  |                | LEF1        |
| 201482_at   | -1.28902191317183 | 0  |                | QSCN6       |
| 217979_at   | 1.28815999568218  | 0  |                | NET-6       |



|                                     |                        |                 |                       |                    |  |
|-------------------------------------|------------------------|-----------------|-----------------------|--------------------|--|
| <b>ALL B not Ph vs. AML t(8;21)</b> |                        | samples: 9 / 13 |                       |                    |  |
| accuracy                            | 1                      |                 |                       |                    |  |
| confidence                          | 1                      |                 |                       |                    |  |
| <b>gene</b>                         | <b>signal-to-noise</b> | <b>p</b>        | <b>decision limit</b> | <b>gene symbol</b> |  |
| 202382_s_at                         | -2.19898458962526      | 0*              | 48.7                  | GNPI               |  |
| 230441_at                           | 2.03717805375485       | 0               |                       |                    |  |
| 228827_at                           | -2.03460798747208      | 0               |                       |                    |  |
| 219478_at                           | -1.99876002437156      | 0               |                       | WFDC1              |  |
| 218718_at                           | -1.92298631566524      | 0               |                       | PDGFC              |  |
| 203795_s_at                         | 1.88483347573406       | 0               |                       | BCL7A              |  |
| 229487_at                           | 1.78170685853126       | 0               |                       |                    |  |
| 241383_at                           | -1.74636612447809      | 0               |                       |                    |  |
| 236656_s_at                         | 1.74257382856431       | 0               |                       |                    |  |
| 235818_at                           | -1.70111545046162      | 0               |                       |                    |  |
| 239278_at                           | 1.69632987254595       | 0               |                       |                    |  |
| 204647_at                           | -1.69400429479148      | 0               |                       | HOMER-3            |  |
| 213944_x_at                         | 1.69297405468728       | 0               |                       |                    |  |
| 217989_at                           | -1.69293289781308      | 0               |                       | LOC51170           |  |
| 205528_s_at                         | -1.64467496425566      | 0               |                       | CBFA2T1            |  |
| 38269_at                            | 1.6387714295779        | 0               |                       | PKD2               |  |
| 201644_at                           | 1.59860594123581       | 0               |                       | TSTA3              |  |
| 206622_at                           | -1.58757343463781      | 0               |                       | TRH                |  |
| 204319_s_at                         | -1.57313966435531      | 0               |                       | RGS10              |  |

|                      |                     |                   |                |               |
|----------------------|---------------------|-------------------|----------------|---------------|
| ALL Ph vs. all other |                     | samples: 15 / 254 |                |               |
| accuracy             | 0.973977695167286   |                   |                |               |
| confidence           | 1                   |                   |                |               |
| failed:              | 5,6,10,12,13,14,139 |                   |                |               |
| gene                 | signal-to-noise     | p                 | decision limit | gene symbol   |
| 210487_at            | 1.46744760454294    | 0                 |                | DNTT          |
| 203373_at            | 1.40251061555498    | 0                 |                | STAT12        |
| 234107_s_at          | -1.30126819904145   | 0                 |                |               |
| 224772_at            | 1.2067398887062     | 0                 |                | MGC14961      |
| 201540_at            | 1.17259032247018    | 0                 |                | FHL1          |
| 202123_s_at          | 1.11803958640816    | 0                 |                | ABL1          |
| 202052_s_at          | 1.1015960943329     | 0                 |                | RAI14         |
| 207971_s_at          | 1.09522659077439    | 0                 |                | KIAA0582      |
| 218589_at            | 1.08650464406846    | 0                 |                | P2Y5          |
| 210299_s_at          | 1.08531672501274    | 0                 |                | FHL1          |
| 227584_at            | 1.05386625392045    | 0                 |                |               |
| 223314_at            | 1.04772672325566    | 0                 |                | MGC11352      |
| 203355_s_at          | 1.04604188199321    | 0                 |                | KIAA0942      |
| 212975_at            | 1.04561133965056    | 0                 |                | KIAA0870      |
| 214505_s_at          | 1.03851430654898    | 0                 |                | FHL1          |
| 222154_s_at          | 1.03658126355559    | 0                 |                | DKFZP564A2416 |
| 209679_s_at          | 1.00639728893477    | 0                 |                | LOC57228      |
| 230659_at            | 1.0054326445936     | 0                 |                | KIAA0212      |
| 1007_s_at            | 1.00231733413632    | 0                 |                | DDR1          |
| 227998_at            | 0.995615703854239   | 0*                | 3687.45        | MGC17528      |

**ALL Ph vs. T-ALL**

samples: 15 / 9

| accuracy    | 1                 |    |                |             |
|-------------|-------------------|----|----------------|-------------|
| confidence  | 1                 |    |                |             |
| gene        | signal-to-noise   | p  | decision limit | gene symbol |
| 218224_at   | -2.4418494296856  | 0  |                | PNMA1       |
| 213854_at   | 2.14963630962421  | 0  |                | SYNGR1      |
| 221969_at   | 2.06978634038245  | 0* | 152.35         | PAX5        |
| 205101_at   | 1.84182814954198  | 0  |                | MHC2TA      |
| 213539_at   | -1.83994967875006 | 0  |                | CD3D        |
| 228988_at   | -1.79658055608971 | 0  |                | ZNF6        |
| 208894_at   | 1.79489847703276  | 0  |                | HLA-DRA     |
| 209604_s_at | -1.75648531255811 | 0  |                | GATA3       |
| 209619_at   | 1.72743796589982  | 0  |                | CD74        |
| 209771_x_at | 1.69086499548436  | 0  |                | CD24        |
| 210982_s_at | 1.68104679025052  | 0  |                | HLA-DRA     |
| 229487_at   | 1.66237077940113  | 0  |                |             |
| 235706_at   | 1.65050775066494  | 0  |                | CPM         |
| 226878_at   | 1.64629305544324  | 0  |                |             |
| 219631_at   | -1.6447182870532  | 0  |                | FLJ12929    |
| 216379_x_at | 1.61950446576807  | 0  |                |             |
| 232234_at   | -1.6009007845449  | 0  |                | C20orf24    |
| 210116_at   | -1.58593866198308 | 0  |                | SH2D1A      |
| 224772_at   | 1.58464619249453  | 0  |                | MGC14961    |
| 213944_x_at | 1.58085800202538  | 0  |                |             |

|                          |                        |                  |                       |                    |
|--------------------------|------------------------|------------------|-----------------------|--------------------|
| <b>ALL Ph vs. AML +8</b> |                        | samples: 15 / 10 |                       |                    |
| accuracy                 | 1                      |                  |                       |                    |
| confidence               | 1                      |                  |                       |                    |
| <b>gene</b>              | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 210487_at                | 2.5237441884906        | 0                |                       | DNTT               |
| 203373_at                | 1.87201491464778       | 0                |                       | STAT2              |
| 202626_s_at              | -1.85118734150368      | 0                |                       | LYN                |
| 226545_at                | 1.80654821675707       | 0                |                       |                    |
| 219229_at                | -1.75947760308609      | 0                |                       | SLC21A11           |
| 201828_x_at              | -1.75807186867031      | 0                |                       | CXX1               |
| 217979_at                | 1.75748092515514       | 0                |                       | NET-6              |
| 51192_at                 | -1.7460030120736       | 0                |                       | SSH-3              |
| 229302_at                | 1.73677596348294       | 0                |                       |                    |
| 226438_at                | -1.70384127791425      | 0                |                       |                    |
| 227367_at                | -1.69193353561271      | 0                |                       |                    |
| 229487_at                | 1.66237077940113       | 0                |                       |                    |
| 234107_s_at              | -1.64136875764363      | 0*               | 340.6                 |                    |
| 204672_s_at              | -1.64125970689002      | 0                |                       | ANKRD6             |
| 202625_at                | -1.61126391589076      | 0                |                       | LYN                |
| 231887_s_at              | 1.60675392068253       | 0                |                       | KIAA1274           |
| 218942_at                | -1.59127524427508      | 0                |                       | FLJ22055           |
| 210749_x_at              | 1.58213182698513       | 0                |                       | DDR1               |
| 213150_at                | -1.57881564631984      | 0                |                       | HOXA10             |
| 59697_at                 | 1.03007856466368       | 0                |                       |                    |

|                        |                   |                  |                |              |
|------------------------|-------------------|------------------|----------------|--------------|
| ALL Ph vs. AML complex |                   | samples: 15 / 36 |                |              |
| accuracy               | 0.980392156862745 |                  |                |              |
| confidence             | 1                 |                  |                |              |
| failed:                | 41                |                  |                |              |
| gene                   | signal-to-noise   | p                | decision limit | gene symbol  |
| 203373_at              | 2.31025004347829  | 0                | 250.95         | STATI2       |
| 206847_s_at            | -1.68023930751716 | 0                |                | HOXA7        |
| 203372_s_at            | 1.63947005879125  | 0                |                | STATI2       |
| 234107_s_at            | -1.61839900546276 | 0                |                |              |
| 210487_at              | 1.52754184797369  | 0                |                | DNTT         |
| 214651_s_at            | -1.49910544616071 | 0*               |                | HOXA9        |
| 209619_at              | 1.49461107113623  | 0                |                | CD74         |
| 218718_at              | -1.42002659230416 | 0                |                | PDGFC        |
| 225660_at              | 1.39520949215218  | 0                |                | SEMA6A       |
| 226878_at              | 1.38541949367152  | 0                |                |              |
| 235753_at              | -1.36744735557489 | 0                |                |              |
| 229817_at              | 1.35899260632582  | 0                |                | DKFZP434M098 |
| 229487_at              | 1.334779526707    | 0                |                |              |
| 214761_at              | 1.33168680907428  | 0                |                | OAZ          |
| 225782_at              | -1.32289994708003 | 0                |                |              |
| 209905_at              | -1.31131029251837 | 0                |                | HOXA9        |
| 235521_at              | -1.3094635283322  | 0                |                | HOXA3        |
| 221969_at              | 1.30539974000703  | 0                |                | PAX5         |
| 213150_at              | -1.28908316992088 | 0                |                | HOXA10       |
| 243363_at              | 1.22268997650812  | 0                |                | LEF1         |

|                              |                        |                  |                       |                    |  |
|------------------------------|------------------------|------------------|-----------------------|--------------------|--|
| <b>ALL Ph vs. AML normal</b> |                        | samples: 15 / 62 |                       |                    |  |
| accuracy                     | 1                      |                  |                       |                    |  |
| confidence                   | 0.974929287250918      |                  |                       |                    |  |
| <b>gene</b>                  | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |  |
| 214651_s_at                  | -1.85202940734635      | 0*               | 143.55                | HOXA9              |  |
| 203373_at                    | 1.62915723435284       | 0                |                       | STAT12             |  |
| 234107_s_at                  | -1.59102595714414      | 0                |                       |                    |  |
| 229817_at                    | 1.58719561744707       | 0                |                       | DKFZP434M098       |  |
| 235753_at                    | -1.57582123676185      | 0                |                       |                    |  |
| 224772_at                    | 1.55894528337306       | 0                |                       | MGC14961           |  |
| 210487_at                    | 1.55488151717647       | 0                |                       | DNTT               |  |
| 212012_at                    | 1.4856092975255        | 0                |                       | D2S448             |  |
| 223449_at                    | 1.48450202420019       | 0                |                       | SEMA6A             |  |
| 209905_at                    | -1.46906077761321      | 0                |                       | HOXA9              |  |
| 213150_at                    | -1.46604197311664      | 0                |                       | HOXA10             |  |
| 212975_at                    | 1.45775514780451       | 0                |                       | KIAA0870           |  |
| 221969_at                    | 1.42534915280476       | 0                |                       | PAX5               |  |
| 206847_s_at                  | -1.42447895990314      | 0                |                       | HOXA7              |  |
| 214761_at                    | 1.42199062015385       | 0                |                       | OAZ                |  |
| 229487_at                    | 1.42117416701658       | 0                |                       |                    |  |
| 217979_at                    | 1.40224984357617       | 0                |                       | NET-6              |  |
| 225660_at                    | 1.39520949215218       | 0                |                       | SEMA6A             |  |
| 212013_at                    | 1.38743332601863       | 0*               | 595.1                 | D2S448             |  |
| 223314_at                    | 1.38610020402626       | 0                |                       | MGC11352           |  |

|                               |                        |                  |                       |                    |
|-------------------------------|------------------------|------------------|-----------------------|--------------------|
| <b>ALL Ph vs. AML t(8;21)</b> |                        | samples: 15 / 13 |                       |                    |
| accuracy                      | 1                      |                  |                       |                    |
| confidence                    | 1                      |                  |                       |                    |
| <b>gene</b>                   | <b>signal-to-noise</b> | <b>p</b>         | <b>decision limit</b> | <b>gene symbol</b> |
| 210487_at                     | 2.25266231447204       | 0                |                       | DNTT               |
| 203373_at                     | 2.24099300433703       | 0                |                       | STAT12             |
| 228827_at                     | -2.03460798747208      | 0*               | 162.15                |                    |
| 226545_at                     | 1.91066898371188       | 0                |                       |                    |
| 224928_at                     | 1.88688841526862       | 0                |                       |                    |
| 218718_at                     | -1.86717048634787      | 0                |                       | PDGFC              |
| 221581_s_at                   | 1.85128137775803       | 0                |                       | WBSCR5             |
| 201811_x_at                   | 1.82001958474325       | 0                |                       | SH3BP5             |
| 201486_at                     | 1.78302051564335       | 0                |                       | RCN2               |
| 207655_s_at                   | 1.77674162168543       | 0                |                       | BLNK               |
| 223467_at                     | 1.77014181133384       | 0                |                       | RASD1              |
| 224764_at                     | 1.76474506640734       | 0                |                       | ARHGAP10           |
| 218237_s_at                   | 1.7513955350881        | 0                |                       | SLC38A1            |
| 212535_at                     | 1.73463136017207       | 0                |                       |                    |
| 202123_s_at                   | 1.72757337414589       | 0                |                       | ABL1               |
| 50221_at                      | 1.71143815565141       | 0                |                       |                    |
| 202600_s_at                   | 1.69190236878682       | 0                |                       | NRIP1              |
| 208146_s_at                   | 1.67349162864443       | 0                |                       | CPVL               |
| 210151_s_at                   | 1.66867162916475       | 0                |                       | DYRK3              |
| 229487_at                     | 1.66237077940113       | 0                |                       |                    |

**T-ALL vs. all other**

samples: 9 / 260

accuracy 0.988847583643123

confidence 0.974096654425726

failed: 2,8,239

| gene        | signal-to-noise   | p  | decision limit | gene symbol |
|-------------|-------------------|----|----------------|-------------|
| 213539_at   | 1.47540002688666  | 0  |                | CD3D        |
| 230588_s_at | 1.40173530720654  | 0  |                | MCPR        |
| 209604_s_at | 1.29998211445613  | 0* | 1756.45        | GATA3       |
| 233589_x_at | -1.29177430222739 | 0* | 1              |             |
| 201416_at   | 1.28847513298777  | 0  |                | SOX4        |
| 228988_at   | 1.22715826655642  | 0  |                | ZNF6        |
| 205640_at   | -1.20119307753531 | 0  |                | ALDH3B1     |
| 201417_at   | 1.20045529988474  | 0  |                |             |
| 228174_at   | 1.19343398440307  | 0  |                |             |
| 206804_at   | 1.19196138585152  | 0  |                | CD3G        |
| 218913_s_at | -1.18780274620161 | 0  |                | LOC51291    |
| 221188_s_at | -1.17857568967097 | 0  |                | CIDEB       |
| 221555_x_at | -1.15605774789743 | 0  |                | CDC14B      |
| 229280_s_at | 1.14891159995685  | 0  |                |             |
| 219079_at   | -1.1401640005663  | 0  |                | b5&b5R      |
| 228242_at   | 1.13931660332537  | 0  |                |             |
| 225003_at   | -1.13574793214416 | 0  |                | MBC3205     |
| 205504_at   | -1.1269796752374  | 0  |                | BTK         |
| 209499_x_at | -1.12273253976539 | 0  |                | TNFSF13     |
| 226342_at   | 1.11835127434314  | 0  |                |             |



| T-ALL vs. AML +8 |                   | samples: 9 / 10 |                |             |  |
|------------------|-------------------|-----------------|----------------|-------------|--|
| accuracy         | 1                 |                 |                |             |  |
| confidence       | 1                 |                 |                |             |  |
| gene             | signal-to-noise   | p               | decision limit | gene symbol |  |
| 233589_x_at      | -5.40566971880279 | 0*              | 94.05          |             |  |
| 211495_x_at      | -3.24639126977955 | 0               |                | TNFSF13     |  |
| 209499_x_at      | -2.48173374690971 | 0               |                | TNFSF13     |  |
| 201416_at        | 2.45175574451932  | 0               |                | SOX4        |  |
| 227999_at        | -2.41422896946156 | 0               |                | LOC170394   |  |
| 205640_at        | -2.36735951723515 | 0               |                | ALDH3B1     |  |
| 218913_s_at      | -2.26146566262815 | 0               |                | LOC51291    |  |
| 242292_at        | 2.13276982228889  | 0               |                |             |  |
| 227729_at        | 2.11399761533966  | 0               |                |             |  |
| 206295_at        | -2.10263843038377 | 0               |                | IL18        |  |
| 218341_at        | -2.09693358964157 | 0               |                | FLJ11838    |  |
| 217989_at        | -2.01015824384982 | 0               |                | LOC51170    |  |
| 201200_at        | -1.9921136873539  | 0               |                | CREG        |  |
| 202626_s_at      | -1.97579203488485 | 0               |                | LYN         |  |
| 201417_at        | 1.94726816387174  | 0               |                |             |  |
| 201985_at        | -1.9229605331952  | 0               |                | KIAA0196    |  |
| 219013_at        | -1.91889126390119 | 0               |                | FLJ21634    |  |
| 219329_s_at      | -1.91383490407803 | 0               |                | APR-3       |  |
| 230588_s_at      | 1.87407116981284  | 0               |                | MCPR        |  |
| 39650_s_at       | 1.68662830524108  | 0               |                | KIAA0435    |  |

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